



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 168510

TO: Bennett Celsa
Location: REM-2A252C18
Art Unit: 1639
Monday, July 11, 2005
Case Serial Number: 09/748739

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Celsa,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

This Page Blank (uspto)

FMS 8

1/8 02p
158510
Access DB#

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: BENNETT CELSA Examiner #: 73815 Date: 7/9/05
Art Unit: 1139 Phone Number 305-7556 Serial Number: 09/748,739
Mail Box and Bldg/Room Location: REMSEN Results Format Preferred (circle): PAPER DISK E-MAIL
2018

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched, include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Butyryl choline esterase Inhibitor

Inventors (please provide full names):

Earliest Priority Filing Date:

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

PERFORM

SEQ SEARCH

1. 29-602 SEQ ID #2

wherein position 356 = Tryptophan (w)

Please note: Seq ID 2 already has tryptophan at 356. No editing

2. INTERf SEARCH was required.

29-602 SEQ ID #2

356 → TRYPTOPHAN

see ATTACHED claim 1

Please Rush

I approve

Mr
JEFFREY FREDMAN
PRIMARY EXAMINER

thanks

Ex CELSR

This Page Blank (uspto)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2005, 11:11:07 ; Search time 77 Seconds
(without alignments)
2883.123 Million cell updates/sec

Title: US-09-748-739A-2_COPY_29_602

Perfect score: 3110

Sequence: 1 EDDIIATKNGKVRGNLTV.....MDWNQFNDFYTSKESCVGL 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A: Genesep 16Dec04: *
1: Genesep1980s: *
2: Genesep1990s: *
3: Genesep2000s: *
4: Genesep2001s: *
5: Genesep2002s: *
6: Genesep2003as: *
7: Genesep2003bs: *
8: Genesep2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3110	100.0	574	7	ABW00722 Human but
2	3110	100.0	602	5	AAO18977 Human but
3	3107	99.9	574	8	ADRO1039 Human but
4	3103	99.8	574	8	ADRO1047 Human but
5	3102	99.7	574	8	ADRO1051 Human but
6	3102	99.7	574	8	ADRO1035 Human but
7	3101	99.7	574	8	ADRO1041 Human but
8	3100	99.7	574	8	ADRO1037 Human but
9	3099	99.6	574	5	AAO18944 Human but
10	3098	99.6	574	8	ADRO1049 Human but
11	3096	99.5	574	5	AAE25235 Human but
12	3096	99.5	574	5	AAO18982 Human but
13	3096	99.5	574	5	AAO18988 Human but
14	3096	99.5	574	6	ABR62391 Human but
15	3096	99.5	574	7	ABW00695 Human but
16	3096	99.5	574	8	ADP44639 Human but
17	3096	99.5	574	8	ADRO1077 Human but
18	3096	99.5	602	3	AAV59235 Human but
19	3096	99.5	602	3	AAV49471 Human but
20	3096	99.5	602	3	AAV44573 Human but
21	3096	99.5	602	6	ABR62392 Human but
22	3096	99.5	602	7	ADP90908 Human but
23	3095	99.5	574	8	ADRO1045 Human but
24	3093	99.5	574	8	ADRO1059 Human but
25	3093	99.5	574	8	ADRO1075 Human but

26	3092	99.4	574	5	AAO18977 Human but
27	3092	99.4	574	7	ABW00722 Human but
28	3092	99.4	574	8	ADRO1080 Human but
29	3092	99.4	602	3	AAV44574 Human but
30	3091	99.4	574	5	AAO18979 Human but
31	3091	99.4	574	5	AAO18980 Human but
32	3091	99.4	602	3	AAV49483 Human but
33	3090	99.4	574	5	AAO18983 Human but
34	3090	99.4	574	5	AAO18945 Human but
35	3090	99.4	574	8	ADP44833 Human but
36	3090	99.4	574	8	ADRO1073 Human but
37	3090	99.4	602	2	AAE37442 Full-length
38	3089	99.3	574	5	AAO18981 Human but
39	3089	99.3	574	5	AAO18940 Human but
40	3089	99.3	574	8	ADRO1079 Human but
41	3089	99.3	574	8	ADRO1078 Human but
42	3089	99.3	602	3	AAV49474 Human but
43	3089	99.3	602	3	AAV49473 Human but
44	3089	99.3	602	3	AAV49475 Human but
45	3088	99.3	574	7	ABW00724 Human but

ALIGNMENTS

RESULT 1

ABW00722
ID ABW00722 standard; protein; 574 AA.

XX AC ABW00722;

XX DT 15-JAN-2004 (first entry)

XX DE Human butyrylcholinesterase variant protein (A328W).

XX KW Human; butyrylcholinesterase; enzyme; mutant; mutein; variant.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 328

XX FT /note= "Wild-type Ala substituted with Trp"

XX PN US2003096401-A1.

XX PD 22-MAY-2003.

XX PF 28-NOV-2001; 2001US-00997209.

XX PR 28-NOV-2000; 2000US-0367370P.

XX PA (HUSE/) HUSE W D.

XX PI Huse WD;

XX XX WPI; 2003-786991/74.

XX PT Cell composition comprises non-yeast eukaryotic cells having diverse population of variant nucleic acids or heterologous nucleic acid fragments, useful for identifying polypeptide with optimized activity.

XX PS Example 11; Page; Opp; English.

XX CC The invention relates to a cell composition comprising a population of non-yeast eukaryotic cells containing diverse population of variant nucleic acids, or heterologous nucleic acid fragments with distinct species of nucleic acid fragments, where each of the variant nucleic acids or heterologous nucleic acid fragments are expressed in different cell and located within each cell at an identical site in the genome. The invention is useful for identifying polypeptide with optimised activity and for identifying a polypeptide receptor for a ligand. The present sequence is human butyrylcholinesterase variant protein. This sequence is

CC used in the exemplification of the invention. Note: This sequence is not
CC shown in the specification but is derived from the human
CC butyrylcholinesterase wild-type protein (ABW0695) shown in figure 8 of
CC the specification
XX
SQ Sequence 574 AA;

Query Match 100.0%; Score 3110; DB 7; Length 574;
Best Local Similarity 100.0%; Pred. No. 2.3e-278; Indels 0; Gaps 0;
Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EDDIIITKNGKVRGMNLTVFSGTTFAPLGIPIYAQPPLGRFRFKKQSLTKWSDIWNATK 60
Db 1 EDDIIITKNGKVRGMNLTVFSGTTFAPLGIPIYAQPPLGRFRFKKQSLTKWSDIWNATK 60
Qy 61 YANSCCNIDQSPFGHSEMNNTDLSDCILYNWIPAPKPKNATVLIWYGGGFQT 120
Db 61 YANSCCNIDQSPFGHSEMNNTDLSDCILYNWIPAPKPKNATVLIWYGGGFQT 120
Qy 121 GTSSLHVYDGFARVERVIVSMNRYRGALGFALPAGNMGLEDDQALQWVOK 180
Db 121 GTSSLHVYDGFARVERVIVSMNRYRGALGFALPAGNMGLEDDQALQWVOK 180
Qy 181 NIAAFGGNPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Db 181 NIAAFGGNPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Qy 241 NRTLNKLATGCSRENETEIIKCLRNDKDPQIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
Db 241 NRTLNKLATGCSRENETEIIKCLRNDKDPQIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
Qy 301 DMPDILLELQGFKKTQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360
Db 301 DMPDILLELQGFKKTQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360
Qy 361 VSEFGKESILPHYTDWDDQRPENYREALGDVVDYFNFCPALFTKTFSEWGNNAFFYY 420
Db 361 VSEFGKESILPHYTDWDDQRPENYREALGDVVDYFNFCPALFTKTFSEWGNNAFFYY 420
Qy 421 FEHRSSKLPWPBWGMVGMHGYEIEFVGLPLERRDNYTKAEIILSRISVKRWANFAKYNP 480
Db 421 FEHRSSKLPWPBWGMVGMHGYEIEFVGLPLERRDNYTKAEIILSRISVKRWANFAKYNP 480
Qy 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOQCRFWTSFFPKVLEMTGNIDEAE 540
Db 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOQCRFWTSFFPKVLEMTGNIDEAE 540
Qy 541 WEWKAGFHRWNNYMDWKNQFNNDYTSKESCVGL 574
Db 541 WEWKAGFHRWNNYMDWKNQFNNDYTSKESCVGL 574

RESULT 2
AAO18897
ID AAO18897 standard; protein; 602 AA.
XX
XX
AC AAO18897;
XX
DT 02-DEC-2002 (first entry)
XX
XX Human butyrylcholinesterase variant #1.
DE
DE Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;
KW cocaine addiction; antiaddictive; antidote.
KW
OS Homo sapiens.
XX
XX WO200264796-A2.
XX
XX 22-AUG-2002.
XX
XX 21-DEC-2001; 2001WO-US050450.
PF
XX

PR 26-DEC-2000; 2000US-00748739.
PR 20-DEC-2001; 2001US-00032233.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
PA (UYNE-) UNIV NEBRASKA MEDICAL CENT.
XX
XX Lockridge O, Watkins JD, Pancook JD;
PI
XX MPI; 2002-636633/68.
DR N-PSDB; AAL49276.
XX
XX New human butyrylcholinesterase variant polypeptides, useful for treating
PT cocaine-induced conditions.
XX
XX Claim 1; Fig 1; 150pp; English.
XX
CC The present invention relates to mutants of human butyrylcholinesterase.
CC The enzymes have an increased cocaine hydrolysis activity and can be used
CC for treating a cocaine-induced condition. The present sequence is a
CC protein shown in the exemplification of the invention
XX
SQ Sequence 602 AA;

Query Match 100.0%; Score 3110; DB 5; Length 602;
Best Local Similarity 100.0%; Pred. No. 2.5e-278;
Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EDDIIITKNGKVRGMNLTVFSGTTFAPLGIPIYAQPPLGRFRFKKQSLTKWSDIWNATK 60
Db 29 EDDIIITKNGKVRGMNLTVFSGTTFAPLGIPIYAQPPLGRFRFKKQSLTKWSDIWNATK 88
Qy 61 YANSCCNIDQSPFGHSEMNNTDLSDCILYNWIPAPKPKNATVLIWYGGGFQT 120
Db 89 YANSCCNIDQSPFGHSEMNNTDLSDCILYNWIPAPKPKNATVLIWYGGGFQT 148
Qy 121 GTSSLHVYDGFARVERVIVSMNRYRGALGFALPAGNMGLEDDQALQWVOK 180
Db 149 GTSSLHVYDGFARVERVIVSMNRYRGALGFALPAGNMGLEDDQALQWVOK 208
Qy 181 NIAAFGGNPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Db 209 NIAAFGGNPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 268
Qy 241 NRTLNKLATGCSRENETEIIKCLRNDKDPQIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
Db 269 NRTLNKLATGCSRENETEIIKCLRNDKDPQIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 328
Qy 301 DMPDILLELQGFKKTQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360
Db 329 DMPDILLELQGFKKTQILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 388
Qy 361 VSEFGKESILPHYTDWDDQRPENYREALGDVVDYFNFCPALFTKTFSEWGNNAFFYY 420
Db 389 VSEFGKESILPHYTDWDDQRPENYREALGDVVDYFNFCPALFTKTFSEWGNNAFFYY 448
Qy 421 FEHRSSKLPWPBWGMVGMHGYEIEFVGLPLERRDNYTKAEIILSRISVKRWANFAKYNP 480
Db 449 FEHRSSKLPWPBWGMVGMHGYEIEFVGLPLERRDNYTKAEIILSRISVKRWANFAKYNP 508
Qy 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOQCRFWTSFFPKVLEMTGNIDEAE 540
Db 509 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAOQCRFWTSFFPKVLEMTGNIDEAE 568
Qy 541 WEWKAGFHRWNNYMDWKNQFNNDYTSKESCVGL 574
Db 569 WEWKAGFHRWNNYMDWKNQFNNDYTSKESCVGL 602

RESULT 3
ADRO1039
ID ADRO1039 standard; protein; 574 AA.
XX
XX AC ADRO1039;

XX DT 23-SEP-2004 (first entry)
XX DE Human butyrylcholinesterase A328W/V331L variant.
XX KW butyrylcholinesterase; cocaine-induced condition;
XX KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
XX KW cocaine addiction; human; butyrylcholinesterase variant.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2004121970-A1.
XX PD 24-JUN-2004.
XX PF 20-DEC-2002; 2002US-00324466.
XX PR 20-DEC-2002; 2002US-00324466.
XX PA (WATK/) WATKINS J D.
XX PA (PANC/) PANCOOK J D.
XX PI Watkins JD, Pancook JD;
XX WPI; 2004-468195/44.
XX DR N-PSDB; ADR01038.
XX DT New butyrylcholinesterase variant polypeptide, useful in treating cocaine
XX PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
XX PS Claim 1; SEQ ID NO 6; 131pp; English.
XX CC The invention describes a butyrylcholinesterase variant polypeptide (I)
XX CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
XX CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
XX CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
XX CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
XX CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
XX CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
XX CC polypeptide comprising any of the 21 sequences of 57 amino acids each
XX CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
XX CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
XX CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
XX CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
XX CC cocaine addiction. This is the amino acid sequence of a human
XX CC butyrylcholinesterase variant.
XX SQ Sequence 574 AA;
Query Match 99.9%; Score 3107; DB 8; Length 574;
Best Local Similarity 99.8%; Pred. No. 4.4e-278;
Matches 573; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EDDIIATNGKVRGNLTIVFGTGTAFGLIPYAPPLGRFRFKKPSQSLTKWSDIWNATK 60
Db 1 EDDIIATNGKVRGNLTIVFGTGTAFGLIPYAPPLGRFRFKKPSQSLTKWSDIWNATK 60
Qy 61 YANSCCNIDQSPFGHSGEMWNPNTDLSDECLYNVWIPAPKPKNATVLIWYGGGFOT 120
Db 61 YANSCCNIDQSPFGHSGEMWNPNTDLSDECLYNVWIPAPKPKNATVLIWYGGGFOT 120
Qy 121 GTSSLHVYDGFARVERVIVSMYRNVGALGFLALPGNPEAPGNMGLFDQQLALQWVOK 180
Db 121 GTSSLHVYDGFARVERVIVSMYRNVGALGFLALPGNPEAPGNMGLFDQQLALQWVOK 180
Qy 181 NIAAPGPNKSVTLFPGESAGASVSLHLLSPGSHSLFTRAILQSGSFNAPWVTSLYEAR 240
Db 181 NIAAPGPNKSVTLFPGESAGASVSLHLLSPGSHSLFTRAILQSGSFNAPWVTSLYEAR 240
Qy 241 NRTLNLAKTGCSRENETEIIKCLRNDKDPQETLLNEAFVVPYGVTPLSVNFPGTVDGDEL 300
Db 241 NRTLNLAKTGCSRENETEIIKCLRNDKDPQETLLNEAFVVPYGVTPLSVNFPGTVDGDEL 300

Qy 301 DMPDILLELGQFKTKTQILVGNKDEGTWFLVYGAPGFSKDNNSITTRKFEQGLKIFPPG 360
Db 301 DMPDILLELGQFKTKTQILVGNKDEGTWFLVYGAPGFSKDNNSITTRKFEQGLKIFPPG 360
Qy 361 VSEFGKSIILPHYTDWVDDQRPENYREALGDVVDYNFICPALBFTKKFSEWGNNAFFYY 420
Db 361 VSEFGKSIILPHYTDWVDDQRPENYREALGDVVDYNFICPALBFTKKFSEWGNNAFFYY 420
Qy 421 FEHRSSKLPWPEWGMVGHGIEIFVGLPLERRRNYTKAEIILSRISIVKRWANFAKYNP 480
Db 421 FEHRSSKLPWPEWGMVGHGIEIFVGLPLERRRNYTKAEIILSRISIVKRWANFAKYNP 480
Qy 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQOCRFWTFFPKVLEMTGNIDAE 540
Db 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQOCRFWTFFPKVLEMTGNIDAE 540
Qy 541 WEWKAGFHRNNYNNMDKNOFNDYTSKKESCVGL 574
Db 541 WEWKAGFHRNNYNNMDKNOFNDYTSKKESCVGL 574
RESULT 4
ADR01047
ID ADR01047 standard; protein; 574 AA.
XX AC ADR01047;
XX DT 23-SEP-2004 (first entry)
XX DE Human butyrylcholinesterase A328W/S287G/A199S variant.
XX KW butyrylcholinesterase; cocaine-induced condition;
XX KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
XX KW cocaine addiction; human; butyrylcholinesterase variant.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2004121970-A1.
XX PD 24-JUN-2004.
XX PF 20-DEC-2002; 2002US-00324466.
XX PR 20-DEC-2002; 2002US-00324466.
XX PA (WATK/) WATKINS J D.
XX PA (PANC/) PANCOOK J D.
XX PI Watkins JD, Pancook JD;
XX WPI; 2004-468195/44.
XX DR N-PSDB; ADR01046.
XX DT New butyrylcholinesterase variant polypeptide, useful in treating cocaine
XX PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
XX PS Claim 1; SEQ ID NO 14; 131pp; English.
XX CC The invention describes a butyrylcholinesterase variant polypeptide (I)
XX CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
XX CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
XX CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
XX CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
XX CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
XX CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
XX CC polypeptide comprising any of the 21 sequences of 57 amino acids each
XX CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
XX CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
XX CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
XX CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
XX CC cocaine addiction. This is the amino acid sequence of a human

```
CC butyrylcholinesterase variant.
XX
SQ Sequence 574 AA;

Query Match          99.8%; Score 3103; DB 8; Length 574;
Best Local Similarity 99.7%; Pred. No. 1.e-277;
Matches 572; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDDIIATKNGKVRGMNLTVFGGTTAFGLIPYAQPPLGRFRFKKPSQSLTKWSDIWNATK 60
Db 1 EDDIIATKNGKVRGMNLTVFGGTTAFGLIPYAQPPLGRFRFKKPSQSLTKWSDIWNATK 60

Qy 61 YANSCCNIDQSPFGFHGSEMNPNNTLSEDCLYLNWIPAPKPKNATVLIWIYGGGFQT 120
Db 61 YANSCCNIDQSPFGFHGSEMNPNNTLSEDCLYLNWIPAPKPKNATVLIWIYGGGFQT 120

Qy 121 GTSSLHVYDGFKLARVERVIVSMNRYVAGLFGFLALPGNPAAGNMGFLDQQLALQWVQK 180
Db 121 GTSSLHVYDGFKLARVERVIVSMNRYVAGLFGFLALPGNPAAGNMGFLDQQLALQWVQK 180

Qy 181 NIAAFGGNPKSVTLFGESAGAAVSLSHLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Db 181 NIAAFGGNPKSVTLFGESAGAAVSLSHLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

Qy 241 NRTNLAKLTGCSRENETETIIKCLRNDKDPQIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
Db 241 NRTNLAKLTGCSRENETETIIKCLRNDKDPQIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300

Qy 301 DMPDILLBLGQFKTKTQILVGVNKGEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360
Db 301 DMPDILLBLGQFKTKTQILVGVNKGEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360

Qy 361 VSEFGKESILFHYTDWDDQRPENYREALGVVDGYNFICPALFTKKFSEWGNNAFFYY 420
Db 361 VSEFGKESILFHYTDWDDQRPENYREALGVVDGYNFICPALFTKKFSEWGNNAFFYY 420

Qy 421 FEHRSSKLPWPPEWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRISVKRWANFAKYGNP 480
Db 421 FEHRSSKLPWPPEWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRISVKRWANFAKYGNP 480

Qy 481 NETQNNSTSWPVFKSTEOKYLTNTTESTRIMTKLRAQQCRFTWTFPPKVLMTGNIDEAE 540
Db 481 NETQNNSTSWPVFKSTEOKYLTNTTESTRIMTKLRAQQCRFTWTFPPKVLMTGNIDEAE 540

Qy 541 WEWKAGFHRWNNYMDWKNQFNDYTSKESCVGL 574
Db 541 WEWKAGFHRWNNYMDWKNQFNDYTSKESCVGL 574

RESULT 5
ADRO1051
ID ADRO1051 standard; protein; 574 AA.
XX
AC ADRO1051;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human butyrylcholinesterase A328W/F227A variant.
XX
KW butyrylcholinesterase; cocaine-induced condition;
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
KW cocaine addiction; human; butyrylcholinesterase variant.
XX
OS Homo sapiens.
OS Synthetic.
XX
FN US2004121970-A1.
XX
PD 24-JUN-2004.
XX
PF 20-DEC-2002; 2002US-00324466.
XX
PR 20-DEC-2002; 2002US-00324466.

XX (WATK/) WATKINS J D.
PA (PANC/) PANCOOK J D.
XX
XX Watkins JD, Pancook JD;
XX WPI; 2004-468195/44.
DR N-PSDB; ADR01050.
XX
XX New butyrylcholinesterase variant polypeptide, useful in treating cocaine
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
XX
XX Claim 1; SEQ ID NO 18; 131pp; English.
XX
XX The invention describes a butyrylcholinesterase variant polypeptide (I)
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.
XX
SQ Sequence 574 AA;

Query Match          99.7%; Score 3102; DB 8; Length 574;
Best Local Similarity 99.8%; Pred. No. 1.3e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDDIIATKNGKVRGMNLTVFGGTTAFGLIPYAQPPLGRFRFKKPSQSLTKWSDIWNATK 60
Db 1 EDDIIATKNGKVRGMNLTVFGGTTAFGLIPYAQPPLGRFRFKKPSQSLTKWSDIWNATK 60

Qy 61 YANSCCNIDQSPFGFHGSEMNPNNTLSEDCLYLNWIPAPKPKNATVLIWIYGGGFQT 120
Db 61 YANSCCNIDQSPFGFHGSEMNPNNTLSEDCLYLNWIPAPKPKNATVLIWIYGGGFQT 120

Qy 121 GTSSLHVYDGFKLARVERVIVSMNRYVAGLFGFLALPGNPAAGNMGFLDQQLALQWVQK 180
Db 121 GTSSLHVYDGFKLARVERVIVSMNRYVAGLFGFLALPGNPAAGNMGFLDQQLALQWVQK 180

Qy 181 NIAAFGGNPKSVTLFGESAGAAVSLSHLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Db 181 NIAAFGGNPKSVTLFGESAGAAVSLSHLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

Qy 241 NRTNLAKLTGCSRENETETIIKCLRNDKDPQIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
Db 241 NRTNLAKLTGCSRENETETIIKCLRNDKDPQIILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300

Qy 301 DMPDILLBLGQFKTKTQILVGVNKGEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360
Db 301 DMPDILLBLGQFKTKTQILVGVNKGEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360

Qy 361 VSEFGKESILFHYTDWDDQRPENYREALGVVDGYNFICPALFTKKFSEWGNNAFFYY 420
Db 361 VSEFGKESILFHYTDWDDQRPENYREALGVVDGYNFICPALFTKKFSEWGNNAFFYY 420

Qy 421 FEHRSSKLPWPPEWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRISVKRWANFAKYGNP 480
Db 421 FEHRSSKLPWPPEWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRISVKRWANFAKYGNP 480

Qy 481 NETQNNSTSWPVFKSTEOKYLTNTTESTRIMTKLRAQQCRFTWTFPPKVLMTGNIDEAE 540
Db 481 NETQNNSTSWPVFKSTEOKYLTNTTESTRIMTKLRAQQCRFTWTFPPKVLMTGNIDEAE 540

Qy 541 WEWKAGFHRWNNYMDWKNQFNDYTSKESCVGL 574
Db 541 WEWKAGFHRWNNYMDWKNQFNDYTSKESCVGL 574
```


Db 541 WEWKAGFHRWNNYMDWKNQFNNDYTSKESCVGL 574

RESULT 6

ID ADR01035 standard; protein; 574 AA.

XX ADR01035

XX ADR01035

XX ADR01035

DT 23-SEP-2004 (first entry)

DE Human butyrylcholinesterase A328W/Y332M variant.

XX butyrylcholinesterase; cocaine-induced condition;

KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;

KW cocaine addition; human; butyrylcholinesterase variant.

XX Homo sapiens.

OS Synthetic.

XX US2004121970-A1.

XX 24-JUN-2004.

PF 20-DEC-2002; 2002US-00324466.

XX 20-DEC-2002; 2002US-00324466.

XX (WATK/) WATKINS J D.

XX (PANC/) PANCOOK J D.

PI Watkins JD, Pancook JD;

DR WPI: 2004-468195/44.

DR N-PSDB; ADR01034.

XX New butyrylcholinesterase variant polypeptide, useful in treating cocaine

PT -induced condition, i.e. cocaine-overdose or cocaine addiction.

XX Claim 1; SEQ ID NO 2; 131pp; English.

XX The invention describes a butyrylcholinesterase variant polypeptide (I) comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID NOS: 2-42) or their functional fragments. Also described are: a nucleic acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a cocaine-induced condition; and a method of hydrolyzing a cocaine-based butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant polypeptide comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The butyrylcholinesterase variant polypeptides and nucleic acids and methods are useful in treating cocaine-induced condition i.e. cocaine-overdose or cocaine addiction. This is the amino acid sequence of a human butyrylcholinesterase variant.

XX Sequence 574 AA;

Query Match 99.7%; Score 3102; DB 8; Length 574;

Best Local Similarity 99.8%; Pred. No. 1.3e-277;

Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGNLTVFGGTVAFLGIPYAPPLGRFLFKFKPQSLTKWSDIWNATK 60

Db 1 EDDIIATKNGKVRGNLTVFGGTVAFLGIPYAPPLGRFLFKFKPQSLTKWSDIWNATK 60

QY 61 YANSCQNDIQSFPGHSGEMNPNLTDSECLYLNWVWPAPKPNATVLIWYGGGQT 120

Db 61 YANSCQNDIQSFPGHSGEMNPNLTDSECLYLNWVWPAPKPNATVLIWYGGGQT 120

QY 121 GTSSLHVYDGKFLARVERIVVSMRYRVCALGFLALPGNPEAPGNMGLFDQOLALQWQK 180

Db 121 GTSSLHVYDGKFLARVERIVVSMRYRVCALGFLALPGNPEAPGNMGLFDQOLALQWQK 180

QY 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

Db 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

QY 241 NRTNLAKLTGCSRENETEIIKCLRNKDPQELLNEAFVVPVGTPLSYNFGPTVGGDFLT 300

Db 241 NRTNLAKLTGCSRENETEIIKCLRNKDPQELLNEAFVVPVGTPLSYNFGPTVGGDFLT 300

QY 301 DMPDILLELGQFKTKTQILVGVNKGDEGTWFLVYGAPGFSKDNNSIITRKEFQGLKIFPPG 360

Db 301 DMPDILLELGQFKTKTQILVGVNKGDEGTWFLVYGAPGFSKDNNSIITRKEFQGLKIFPPG 360

QY 361 VSEFGKESILFHYTDWDDQRPENYREALGVGDYDNFICPALEBTKKPSWGNNAFFYY 420

Db 361 VSEFGKESILFHYTDWDDQRPENYREALGVGDYDNFICPALEBTKKPSWGNNAFFYY 420

QY 421 FEHRSSKLPWPEWGMVHGIEFVFGPLPERRRDNNTKAEELLSRSIVKRWANFAKYNP 480

Db 421 FEHRSSKLPWPEWGMVHGIEFVFGPLPERRRDNNTKAEELLSRSIVKRWANFAKYNP 480

QY 481 NETQNNSTSWPVFKSTEOKYLTLTNTSTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540

Db 481 NETQNNSTSWPVFKSTEOKYLTLTNTSTRIMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540

QY 541 WEWKAGFHRWNNYMDWKNQFNNDYTSKESCVGL 574

Db 541 WEWKAGFHRWNNYMDWKNQFNNDYTSKESCVGL 574

RESULT 7

ADRO1041

ID ADR01041 standard; protein; 574 AA.

XX AC ADR01041;

XX 23-SEP-2004 (first entry)

DE Human butyrylcholinesterase A328W/Y332S variant.

XX butyrylcholinesterase; cocaine-induced condition;

KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;

KW cocaine addition; human; butyrylcholinesterase variant.

XX Homo sapiens.

OS Synthetic.

XX US2004121970-A1.

XX 24-JUN-2004.

PF 20-DEC-2002; 2002US-00324466.

XX 20-DEC-2002; 2002US-00324466.

XX (WATK/) WATKINS J D.

XX (PANC/) PANCOOK J D.

PI Watkins JD, Pancook JD;

DR WPI: 2004-468195/44.

DR N-PSDB; ADR01040.

XX New butyrylcholinesterase variant polypeptide, useful in treating cocaine

PT -induced condition, i.e. cocaine-overdose or cocaine addiction.

XX Claim 1; SEQ ID NO 8; 131pp; English.

XX The invention describes a butyrylcholinesterase variant polypeptide (I) comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID NOS: 2-42) or their functional fragments. Also described are: a nucleic acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a cocaine-induced condition; and a method of hydrolyzing a cocaine-based butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant polypeptide comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The butyrylcholinesterase variant polypeptides and nucleic acids and methods are useful in treating cocaine-induced condition i.e. cocaine-overdose or cocaine addiction. This is the amino acid sequence of a human butyrylcholinesterase variant.

XX Sequence 574 AA;

Query Match 99.7%; Score 3102; DB 8; Length 574;

Best Local Similarity 99.8%; Pred. No. 1.3e-277;

Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGNLTVFGGTVAFLGIPYAPPLGRFLFKFKPQSLTKWSDIWNATK 60

Db 1 EDDIIATKNGKVRGNLTVFGGTVAFLGIPYAPPLGRFLFKFKPQSLTKWSDIWNATK 60

QY 61 YANSCQNDIQSFPGHSGEMNPNLTDSECLYLNWVWPAPKPNATVLIWYGGGQT 120

Db 61 YANSCQNDIQSFPGHSGEMNPNLTDSECLYLNWVWPAPKPNATVLIWYGGGQT 120

QY 121 GTSSLHVYDGKFLARVERIVVSMRYRVCALGFLALPGNPEAPGNMGLFDQOLALQWQK 180

Db 121 GTSSLHVYDGKFLARVERIVVSMRYRVCALGFLALPGNPEAPGNMGLFDQOLALQWQK 180

CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.
XX
XX Sequence 574 AA;

Query Match 99.7%; Score 3101; DB 8; Length 574;
Best Local Similarity 99.8%; Pred. No. 1.6e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFSGTTFATFLGIPYAQPPLGRURFKKPSQSLTKWSDIWNATK 60
DB 1 EDDIIATKNGKVRGMNLTVFSGTTFATFLGIPYAQPPLGRURFKKPSQSLTKWSDIWNATK 60

QY 61 YANSCCQNIQDSFGFHGSEMNPNLTDLSEDCLYLNWIPAPKPKNATVLIWYGGGFQT 120
DB 61 YANSCCQNIQDSFGFHGSEMNPNLTDLSEDCLYLNWIPAPKPKNATVLIWYGGGFQT 120

QY 121 GTSSLVHYDGFARVERVIVSMNRYVGLGFLALPGNPEAPGNMGLFDQQLALQWVQK 180
DB 121 GTSSLVHYDGFARVERVIVSMNRYVGLGFLALPGNPEAPGNMGLFDQQLALQWVQK 180

QY 181 NIAAFGNGPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
DB 181 NIAAFGNGPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

QY 241 NRTNLAKLTGCSRENETEIIKCLRNDKDPQIILNEAFVVPYGPPLSVNFGPTVDGDFLT 300
DB 241 NRTNLAKLTGCSRENETEIIKCLRNDKDPQIILNEAFVVPYGPPLSVNFGPTVDGDFLT 300

QY 301 DMPDILLGQFKTKTQILVGVNKGDEGTWFLVYGAPGFSKONNSIITRKEFOEGLKIFPPG 360
DB 301 DMPDILLGQFKTKTQILVGVNKGDEGTWFLVYGAPGFSKONNSIITRKEFOEGLKIFPPG 360

QY 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDGYNFICPALEFTKKFSEWGNAPFY 420
DB 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDGYNFICPALEFTKKFSEWGNAPFY 420

QY 421 FEHRSSKLPWPENWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRIIVKRWANFAYGNP 480
DB 421 FEHRSSKLPWPENWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRIIVKRWANFAYGNP 480

QY 481 NETQNNSTSWPVKSTEQKYLTLNTESTRIMTKLRAQOCRFWTSPFPKVLKEMTGNIDEAE 540
DB 481 NETQNNSTSWPVKSTEQKYLTLNTESTRIMTKLRAQOCRFWTSPFPKVLKEMTGNIDEAE 540

QY 541 WEWKAGFHRNNYMDWQNDYTSKESCVGL 574
DB 541 WEWKAGFHRNNYMDWQNDYTSKESCVGL 574

RESULT 8

ADRO1037
ID ADRO1037 standard; protein; 574 AA.
XX
AC ADRO1037;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human butyrylcholinesterase A328W/Y332P variant.
XX
KW butyrylcholinesterase; cocaine-induced condition;
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
KW cocaine addiction; human; butyrylcholinesterase variant.
XX
OS Homo sapiens.
OS Synthetic.

XX US2004121970-A1.
PN 24-JUN-2004.
PD
XX 20-DEC-2002; 2002US-00324466.
PF
XX 20-DEC-2002; 2002US-00324466.
PR
XX (WATK/) WATKINS J D.
PA (PANC/) PANCOOK J D.
FA
XX Watkins JD, Pancook JD;
PI
XX WPI: 2004-468195/44.
DR N-PSDB; ADR01036.
XX
XX New butyrylcholinesterase variant polypeptide, useful in treating cocaine
PT -induced condition, i.e. cocaine-overdose or cocaine addiction.
PT
XX Claim 1; SEQ ID NO 4; 131pp; English.
PS
XX The invention describes a butyrylcholinesterase variant polypeptide (I)
CC comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
CC NOS: 2-42) or their functional fragments. Also described are: a nucleic
CC acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416
CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
CC butyrylcholinesterase substrate. (II) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.
XX
SQ Sequence 574 AA;

Query Match 99.7%; Score 3100; DB 8; Length 574;
Best Local Similarity 99.8%; Pred. No. 2e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFSGTTFATFLGIPYAQPPLGRURFKKPSQSLTKWSDIWNATK 60
DB 1 EDDIIATKNGKVRGMNLTVFSGTTFATFLGIPYAQPPLGRURFKKPSQSLTKWSDIWNATK 60

QY 61 YANSCCQNIQDSFGFHGSEMNPNLTDLSEDCLYLNWIPAPKPKNATVLIWYGGGFQT 120
DB 61 YANSCCQNIQDSFGFHGSEMNPNLTDLSEDCLYLNWIPAPKPKNATVLIWYGGGFQT 120

QY 121 GTSSLVHYDGFARVERVIVSMNRYVGLGFLALPGNPEAPGNMGLFDQQLALQWVQK 180
DB 121 GTSSLVHYDGFARVERVIVSMNRYVGLGFLALPGNPEAPGNMGLFDQQLALQWVQK 180

QY 181 NIAAFGNGPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
DB 181 NIAAFGNGPKSVTLFGESAGAAVSLSHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

QY 241 NRTNLAKLTGCSRENETEIIKCLRNDKDPQIILNEAFVVPYGPPLSVNFGPTVDGDFLT 300
DB 241 NRTNLAKLTGCSRENETEIIKCLRNDKDPQIILNEAFVVPYGPPLSVNFGPTVDGDFLT 300

QY 301 DMPDILLGQFKTKTQILVGVNKGDEGTWFLVYGAPGFSKONNSIITRKEFOEGLKIFPPG 360
DB 301 DMPDILLGQFKTKTQILVGVNKGDEGTWFLVYGAPGFSKONNSIITRKEFOEGLKIFPPG 360

QY 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDGYNFICPALEFTKKFSEWGNAPFY 420
DB 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDGYNFICPALEFTKKFSEWGNAPFY 420

QY 421 FEHRSSKLPWPENWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRIIVKRWANFAYGNP 480
DB 421 FEHRSSKLPWPENWGMVHGVEIEFVFGPLPERRDNYTKAEIILSRIIVKRWANFAYGNP 480

Db 421 FEHRSSKLPWPEWGMVGHGIEFVFGLEPLERRDNYTKAEILSRISIVKRWANFAKYGNP 480
QY 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFPFKVLEMTGNIDEAE 540
Db 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFPFKVLEMTGNIDEAE 540
QY 541 WEWKAGFHRWNNYMDWKQNFNDYTSKKESCVGL 574
Db 541 WEWKAGFHRWNNYMDWKQNFNDYTSKKESCVGL 574

RESULT 9
AAO18944
ID AAO18944 standard; protein; 574 AA.
XX
AC AAO18944;
DT 02-DEC-2002 (first entry)
XX
DE Human butyrylcholinesterase mutant A328W.
XX
KW Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;
KW cocaine addition; antiaddictive; antidote; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 328
FT /note= "wild-type Ala substituted by Trp"
XX
XX WO200264796-A2.
XX
XX 22-AUG-2002.
XX
XX 21-DEC-2001; 2001WO-US050450.
XX
XX 26-DEC-2000; 2000US-00748739.
XX 20-DEC-2001; 2001US-00032233.
XX
XX (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
XX (UYNE-) UNIV NEBRASKA MEDICAL CENT.
XX
XX Lockridge O, Watkins JD, Pancook JD;
XX
XX WPI; 2002-636633/68.
XX
XX
XX New human butyrylcholinesterase variant polypeptides, useful for treating
XX cocaine-induced conditions.
XX
XX Example 1; Page; 150pp; English.
XX
XX The present invention relates to mutants of human butyrylcholinesterase.
XX The enzymes have an increased cocaine hydrolysis activity and can be used
XX for treating a cocaine-induced condition. The present sequence is a
XX mutant protein shown in the exemplification of the invention
XX
XX Sequence 574 AA;
XX

Query Match 99.6%; Score 3099; DB 5; Length 574;
Best Local Similarity 99.8%; Pred. No. 2.4e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EDDIIATKNGKVRGNLTVFGSTVTAFLGIPYAPPLGLRFRKPKQSLTKWSDIWNATK 60
Db 1 EDDIIATKNGKVRGNLTVFGSTVTAFLGIPYAPPLGLRFRKPKQSLTKWSDIWNATK 60
QY 61 YANSCQNDIQSPFGHSEMNPNPDLSDCLYLNWVIPAPKPNATVLIWYGGGQT 120
Db 61 YANSCQNDIQSPFGHSEMNPNPDLSDCLYLNWVIPAPKPNATVLIWYGGGQT 120
QY 121 GTSSLHVVDGKFLARVERIVVSMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVOK 180

Db 121 GTSSLHVVDGKFLARVERIVVSMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVOK 180
QY 181 NIAAFGNGPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPMAVTSLYEAR 240
Db 181 NIAAFGNGPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPMAVTSLYEAR 240
QY 241 NRTLNLAKLTGCSRNETETIILKCLRNKDPQOELLNEAFVVPYGTPLSNFGPTVDGDFLT 300
Db 241 NRTLNLAKLTGCSRNETETIILKCLRNKDPQOELLNEAFVVPYGTPLSNFGPTVDGDFLT 300
QY 301 DMPDILLELGOFKKTQILVGVNKDGTWFLVYGAPGFSKDNNSIITRKEFQEGKIFPPG 360
Db 301 DMPDILLELGOFKKTQILVGVNKDGTWFLVYGAPGFSKDNNSIITRKEFQEGKIFPPG 360
QY 361 VSEFGKESILFHYTDDVDDQRPENYREALGDVVDYFNFCIPALEFTKFSSEGNNAFFYY 420
Db 361 VSEFGKESILFHYTDDVDDQRPENYREALGDVVDYFNFCIPALEFTKFSSEGNNAFFYY 420
QY 421 FEHRSSKLPWPEWGMVGHGIEFVFGLEPLERRDNYTKAEILSRISIVKRWANFAKYGNP 480
Db 421 FEHRSSKLPWPEWGMVGHGIEFVFGLEPLERRDNYTKAEILSRISIVKRWANFAKYGNP 480
QY 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFPFKVLEMTGNIDEAE 540
Db 481 NETQNNSTSWPVFKSTEQKYLTLNTESTRIMTKLRAQQCRFWTSFPFKVLEMTGNIDEAE 540
QY 541 WEWKAGFHRWNNYMDWKQNFNDYTSKKESCVGL 574
Db 541 WEWKAGFHRWNNYMDWKQNFNDYTSKKESCVGL 574

RESULT 10
ADRO1049
ID ADRO1049 standard; protein; 574 AA.
XX
AC ADRO1049;
DT 23-SEP-2004 (first entry)
XX
DE Human butyrylcholinesterase A328W/S287G/F227A variant.
XX
KW butyrylcholinesterase; cocaine-induced condition;
KW cocaine-based butyrylcholinesterase substrate; cocaine-overdose;
KW cocaine addiction; human; butyrylcholinesterase variant.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX US2004121970-A1.
XX
XX 24-JUN-2004.
XX
XX 20-DEC-2002; 2002US-00324466.
XX
XX 20-DEC-2002; 2002US-00324466.
XX
XX (WATK/) WATKINS J D.
XX (PANC/) PANCOOK J D.
XX
XX Watkins JD, Pancook JD;
XX
XX WPI; 2004-468195/44.
XX N-PSDB; ADRO1048.
XX
XX New butyrylcholinesterase variant polypeptide, useful in treating cocaine
XX -induced condition, i.e. cocaine-overdose or cocaine addiction.
XX
XX Claim 1; SEQ ID NO 16; 131pp; English.
XX
XX The invention describes a butyrylcholinesterase variant polypeptide (I)
XX comprising any of the 21 sequences of 57 amino acids each (EVEN SEQ ID
XX NOS: 2-42) or their functional fragments. Also described are: a nucleic
XX acid encoding (I) comprising any of the 21 nucleic acid sequences of 2416

CC bp each (ODD SEQ ID NOS: 1-41) or their fragments; a method of treating a
CC cocaine-induced condition; and a method of hydrolysing a cocaine-based
CC butyrylcholinesterase substrate. (I) is butyrylcholinesterase variant
CC polypeptide comprising any of the 21 sequences of 57 amino acids each
CC (EVEN SEQ ID NOS: 2-42), encoded by a nucleic acid comprising any of the
CC 21 nucleic acid sequences of 2416 bp each (ODD SEQ ID NOS: 1-41). The
CC butyrylcholinesterase variant polypeptides and nucleic acids and methods
CC are useful in treating cocaine-induced condition i.e. cocaine-overdose or
CC cocaine addiction. This is the amino acid sequence of a human
CC butyrylcholinesterase variant.
XX
SQ Sequence 574 AA;

Query Match 99.6%; Score 3098; DB 8; Length 574;
Best Local Similarity 99.7%; Pred. No. 3e-277;
Matches 572; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EDDIIATKNGKVRGMNLTVEGGVTAPLGIPIYAQPPLGRFRKKPQSLTKWSDIWNATK 60
Db 1 EDDIIATKNGKVRGMNLTVEGGVTAPLGIPIYAQPPLGRFRKKPQSLTKWSDIWNATK 60
Qy 61 YANSCCNIDQSPFGFHGSEMNNPNTDLSBCLYLNWVWPAPKPNATVLIWIYGGGQFT 120
Db 61 YANSCCNIDQSPFGFHGSEMNNPNTDLSBCLYLNWVWPAPKPNATVLIWIYGGGQFT 120
Qy 121 GTSSHYVDGKFLARVERVIVSNRYVGALGFLALPKNPEAPGNMGLFDQQLALQWVK 180
Db 121 GTSSHYVDGKFLARVERVIVSNRYVGALGFLALPKNPEAPGNMGLFDQQLALQWVK 180
Qy 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRALQSGSANAPWAVTSLYEAR 240
Db 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRALQSGSANAPWAVTSLYEAR 240
Qy 241 NRTNLAKLTGCSRENETEIIKCLRNDQDQOILLNEAPVVPYGPPLSVNGFPTVGDGFLT 300
Db 241 NRTNLAKLTGCSRENETEIIKCLRNDQDQOILLNEAPVVPYGPPLSVNGFPTVGDGFLT 300
Qy 301 DMPDILLELGQFKTQILLVGNKDEGTWFLVYGAPGSKNNNSIITRKEFOEGLKIFPPG 360
Db 301 DMPDILLELGQFKTQILLVGNKDEGTWFLVYGAPGSKNNNSIITRKEFOEGLKIFPPG 360
Qy 361 VSEFGKESILPHYTDWDDQRPENYREALGDVVDYDFNFCIPALEFTKKFSEWGNNAFFYY 420
Db 361 VSEFGKESILPHYTDWDDQRPENYREALGDVVDYDFNFCIPALEFTKKFSEWGNNAFFYY 420
Qy 421 FEHRSSKLPWPEWGMVHGIEIFVFGPLPERRDNYTKAEIILSRISIVKRWANFAKYNP 480
Db 421 FEHRSSKLPWPEWGMVHGIEIFVFGPLPERRDNYTKAEIILSRISIVKRWANFAKYNP 480
Qy 481 NETQNNSTWVPKSTQKYLTLNTESTRIMTKLRAQOCRFWTSFFPKVLEMTGNIDEAE 540
Db 481 NETQNNSTWVPKSTQKYLTLNTESTRIMTKLRAQOCRFWTSFFPKVLEMTGNIDEAE 540
Qy 541 WEWKAGFHRMNNYMDWKNQFNNDYTSKESCVGL 574
Db 541 WEWKAGFHRMNNYMDWKNQFNNDYTSKESCVGL 574

RESULT 11
AAE25235
ID AAE25235 standard; protein; 574 AA.
XX
AC AAE25235;
XX
DT 30-OCT-2002 (first entry)
XX
DE Human butyrylcholinesterase protein.
XX
KW Human; optimisation; drug; butyrylcholinesterase; enzyme.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers

FT Disulfide-bond 65..92
FT Region 68..82
FT Active-site 82
FT Region 110..121
FT Active-site 112
FT Active-site 128
FT Region 194..201
FT Region 224..234
FT Active-site 231
FT Disulfide-bond 252..263
FT Region 277..289
FT Region 327..332
FT Active-site 329
FT Active-site 332
FT Disulfide-bond 400..519
FT Region 429..442
FT Active-site 430
FT Active-site 440
XX W020024361-A2.
PN 06-JUN-2002.
XX 28-NOV-2001; 2001WO-US044600.
XX 28-NOV-2000; 2000US-00724762.
XX (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
XX Huse WD;
XX WPT; 2002-519586/55.
XX New cell composition having population of non-yeast eukaryotic cells
XX containing diverse population of variant nucleic acids that are expressed
XX in different cell and located within each cell at identical site in
XX genome.
XX Example 11; Page 155-156; 157pp; English.
XX The present invention relates to a cell composition having population of
XX non-yeast eukaryotic cells containing a diverse population of ten or more
XX variant nucleic acids or heterologous nucleic acid fragments comprising
XX distinct species of nucleic acid fragments, each of the variant nucleic
XX acids or heterologous nucleic acid fragments being expressed in different
XX cells and located within each cell at an identical site in the genome.
XX The composition is useful to identify polypeptides exhibiting optimised
XX activity. It is also useful for identifying a binding ligand. It is also
XX useful for identifying specific ligands to desired target molecules. Such
XX ligands can be developed as potential drug candidates or alternatively
XX used as lead compounds for the generation and identification of ligand
XX variants which exhibit enhanced activity of the desired binding property.
XX The methods can similarly be applied to identify a nucleic acid having an
XX optimised activity by screening for an activity associated with a parent
XX nucleic acid. The present sequence is human butyrylcholinesterase
XX protein. This sequence is used in the exemplification of the invention
XX Sequence 574 AA;

Query Match 99.5%; Score 3096; DB 5; Length 574;
Best Local Similarity 99.8%; Pred. No. 4.6e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVEGTTAFGLGIPYAQPPLGRRLRFKKPQSLTKWSDIWNATK 60
DB 1 EDDIIATKNGKVRGMNLTVEGTTAFGLGIPYAQPPLGRRLRFKKPQSLTKWSDIWNATK 60

QY 61 YANSCCQNIQDQSPFGHSEMMNPTDLSDECLYNVWIPAPKPKNATVLIWYGGGQ 120
DB 61 YANSCCQNIQDQSPFGHSEMMNPTDLSDECLYNVWIPAPKPKNATVLIWYGGGQ 120

QY 121 GTSSLHVVDGKFLARVERVIVSMNRYVGAFLALPGNPEAPGNMGLFDQQLALQWVK 180
DB 121 GTSSLHVVDGKFLARVERVIVSMNRYVGAFLALPGNPEAPGNMGLFDQQLALQWVK 180

QY 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
DB 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

QY 241 NRTLNKLATGCSRENETEIIKCLRNKDPQEIILLNEAFVVPYGTPLSVNFGPTVDGDEL 300
DB 241 NRTLNKLATGCSRENETEIIKCLRNKDPQEIILLNEAFVVPYGTPLSVNFGPTVDGDEL 300

QY 301 DMPDILLLELQPKTKTQILVGVNKGDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360
DB 301 DMPDILLLELQPKTKTQILVGVNKGDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360

QY 361 VSEFKESILPHYTDWDDQRPENYREALGDVVDYNTFCPALEFTKKPSEWGNNAFFY 420
DB 361 VSEFKESILPHYTDWDDQRPENYREALGDVVDYNTFCPALEFTKKPSEWGNNAFFY 420

QY 421 FEHRSKLPWPPEWGMVHGVEIEFVGLPLERRDNYTKAEIILSRISIVKRWANFAKYNP 480
DB 421 FEHRSKLPWPPEWGMVHGVEIEFVGLPLERRDNYTKAEIILSRISIVKRWANFAKYNP 480

QY 481 NETQNNSTSWPVFKSTEOKYLTNTSTRTMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540
DB 481 NETQNNSTSWPVFKSTEOKYLTNTSTRTMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540

QY 541 WEWKAGFHRWNNYMDWKNQNDYTSKESCVGL 574
DB 541 WEWKAGFHRWNNYMDWKNQNDYTSKESCVGL 574

RESULT 12

AAO18982
ID AAO18982 standard; protein; 574 AA.

AC AAO18982;

XX 02-DEC-2002 (first entry)

DE Human butyrylcholinesterase mutant A328/V331L.

XX Human; butyrylcholinesterase; enzyme; mutant; cocaine hydrolysis;
KW cocaine addition; antiaddictive; antidote; mutin.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 328

FT /note= "wild-type Ala substituted by Trp"

FT Misc-difference 331

FT /note= "wild-type Val substituted by Leu"

XX WO200264796-A2.

XX 22-AUG-2002.

XX 21-DEC-2001; 2001WO-US050450.

XX AC

XX AAO18982;

XX 26-DEC-2000; 2000US-00748739.
PR 20-DEC-2001; 2001US-00032233.
XX (MOLE-) APPLIED MOLECULAR EVOLUTION INC.
PA (UYNE-) UNIV NEBRASKA MEDICAL CENT.
XX Lockridge O, Watkins JD, Pancook JD;
PI WPI; 2002-636633/68.
XX New human butyrylcholinesterase variant polypeptides, useful for treating
PT cocaine-induced conditions.
XX Claim 1; Page; 150pp; English.
XX The present invention relates to mutants of human butyrylcholinesterase.
CC The enzymes have an increased cocaine hydrolysis activity and can be used
CC for treating a cocaine-induced condition. The present sequence is a
CC mutant protein shown in the exemplification of the invention
XX Sequence 574 AA;

Query Match 99.5%; Score 3096; DB 5; Length 574;

Best Local Similarity 99.7%; Pred. No. 4.6e-277;

Matches 572; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVEGTTAFGLGIPYAQPPLGRRLRFKKPQSLTKWSDIWNATK 60

DB 1 EDDIIATKNGKVRGMNLTVEGTTAFGLGIPYAQPPLGRRLRFKKPQSLTKWSDIWNATK 60

QY 61 YANSCCQNIQDQSPFGHSEMMNPTDLSDECLYNVWIPAPKPKNATVLIWYGGGQ 120

DB 61 YANSCCQNIQDQSPFGHSEMMNPTDLSDECLYNVWIPAPKPKNATVLIWYGGGQ 120

QY 121 GTSSLHVVDGKFLARVERVIVSMNRYVGAFLALPGNPEAPGNMGLFDQQLALQWVK 180

DB 121 GTSSLHVVDGKFLARVERVIVSMNRYVGAFLALPGNPEAPGNMGLFDQQLALQWVK 180

QY 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

DB 181 NIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240

QY 241 NRTLNKLATGCSRENETEIIKCLRNKDPQEIILLNEAFVVPYGTPLSVNFGPTVDGDEL 300

DB 241 NRTLNKLATGCSRENETEIIKCLRNKDPQEIILLNEAFVVPYGTPLSVNFGPTVDGDEL 300

QY 301 DMPDILLLELQPKTKTQILVGVNKGDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360

DB 301 DMPDILLLELQPKTKTQILVGVNKGDEGTWFLVYGAPGFSKDNNSIITRKEFOEGLKIFPPG 360

QY 361 VSEFKESILPHYTDWDDQRPENYREALGDVVDYNTFCPALEFTKKPSEWGNNAFFY 420

DB 361 VSEFKESILPHYTDWDDQRPENYREALGDVVDYNTFCPALEFTKKPSEWGNNAFFY 420

QY 421 FEHRSKLPWPPEWGMVHGVEIEFVGLPLERRDNYTKAEIILSRISIVKRWANFAKYNP 480

DB 421 FEHRSKLPWPPEWGMVHGVEIEFVGLPLERRDNYTKAEIILSRISIVKRWANFAKYNP 480

QY 481 NETQNNSTSWPVFKSTEOKYLTNTSTRTMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540

DB 481 NETQNNSTSWPVFKSTEOKYLTNTSTRTMTKLRAQOCRFWTSFPFKVLEMTGNIDAE 540

QY 541 WEWKAGFHRWNNYMDWKNQNDYTSKESCVGL 574

DB 541 WEWKAGFHRWNNYMDWKNQNDYTSKESCVGL 574

RESULT 13

AAO18898

ID AAO18898 standard; protein; 574 AA.

XX AC

XX AAO18898;


```
QY 121 GTSSLLHYVDGKFLARVERVIVSMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVK 180
Db 121 GTSSLLHYVDGKFLARVERVIVSMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVK 180
QY 181 NIAAFGCGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Db 181 NIAAFGCGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
QY 241 NRTNLAKLTGCSRENETEIIKCLRNKDPQOEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
Db 241 NRTNLAKLTGCSRENETEIIKCLRNKDPQOEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
QY 301 DMPDILILELQKQKTOILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFQSGLKIFPPG 360
Db 301 DMPDILILELQKQKTOILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFQSGLKIFPPG 360
QY 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDYFNFCPALEFTKFSSEGNNAFFYY 420
Db 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDYFNFCPALEFTKFSSEGNNAFFYY 420
QY 421 FEHRSSKLPWPPEWGMVHGIEFVFGFLPERRDNYTKAEIILSRISIVKRWANFAKYGNP 480
Db 421 FEHRSSKLPWPPEWGMVHGIEFVFGFLPERRDNYTKAEIILSRISIVKRWANFAKYGNP 480
QY 481 NETQNNSTSWPVKFSQTEQKYLINTESTRIMTKLRAQQCRFWTSPPPKVLEMTGNIDEAE 540
Db 481 NETQNNSTSWPVKFSQTEQKYLINTESTRIMTKLRAQQCRFWTSPPPKVLEMTGNIDEAE 540
QY 541 WEWKAGFHRWNNYMDKQNDYTSKESCVGL 574
Db 541 WEWKAGFHRWNNYMDKQNDYTSKESCVGL 574

RESULT 15
ID ABW00695
AC ABW00695;
XX
XX
DT 15-JAN-2004 (first entry)
XX
XX Human butyrylcholinesterase protein.
XX Human; butyrylcholinesterase; enzyme.
XX Homo sapiens.
XX
XX Key
XX Location/Qualifiers
FT 68..82
FT /note= "Region used to generate focused libraries of
FT butyrylcholinesterase"
FT 82
FT Active-site
FT 110..121
FT Region
FT /note= "Region used to generate focused libraries of
FT butyrylcholinesterase variants"
FT 112
FT Active-site
FT 128
FT Active-site
FT 194..201
FT Region
FT /note= "Region used to generate focused libraries of
FT butyrylcholinesterase"
FT 224..234
FT Region
FT /note= "Region used to generate focused libraries of
FT butyrylcholinesterase variants"
FT 231
FT Active-site
FT 277..289
FT Region
FT /note= "Region used to generate focused libraries of
FT butyrylcholinesterase variants"
FT 327..332
FT Region
FT /note= "Region used to generate focused libraries of
FT butyrylcholinesterase"
FT 329
FT Active-site
FT 332
FT Active-site
FT 429..442
FT Region
```

```
FT /note= "Region used to generate focused libraries of
FT butyrylcholinesterase variants"
FT 430
FT Active-site
FT 440
XX US2003096401-Al.
XX 22-MAY-2003.
XX 28-NOV-2001; 2001US-00997209.
XX 28-NOV-2000; 2000US-0367370P.
XX (HUSE/) HUSE W D.
XX Huse WD;
XX WPI; 2003-786991/74.
XX
XX Cell composition comprises non-yeast eukaryotic cells having diverse
XX population of variant nucleic acids or heterologous nucleic acid
XX fragments, useful for identifying polypeptide with optimized activity.
XX
XX Example 11; Fig 8; Opp; English.
XX
XX The invention relates to a cell composition comprising a population of
XX non-yeast eukaryotic cells containing diverse population of variant
XX nucleic acids, or heterologous nucleic acid fragments with distinct
XX species of nucleic acid fragments, where each of the variant nucleic
XX acids or heterologous nucleic acid fragments are expressed in different
XX cell and located within each cell at an identical site in the genome. The
XX invention is useful for identifying polypeptide with optimised activity
XX and for identifying a polypeptide receptor for a ligand. The present
XX sequence is human butyrylcholinesterase protein. This sequence is used in
XX the exemplification of the invention
XX
XX Sequence 574 AA;
```

```
Query Match 99.5%; Score 3096; DB 7; Length 574;
Best Local Similarity 99.8%; Pred. No. 4.6e-277;
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 EDDIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPLGLRFLFKPQSLTKWSDIWNATK 60
Db 1 EDDIIATKNGKVRGMNLTVFGGTVTAFLGIPYAQPLGLRFLFKPQSLTKWSDIWNATK 60
QY 61 YANSCCQNDIOSFPGFHGSEMMNPNTDISEDCLYLNWIPAPKPNATVLIWYGGFOT 120
Db 61 YANSCCQNDIOSFPGFHGSEMMNPNTDISEDCLYLNWIPAPKPNATVLIWYGGFOT 120
QY 121 GTSSLLHYVDGKFLARVERVIVSMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVK 180
Db 121 GTSSLLHYVDGKFLARVERVIVSMYRVGALGFLALPGNPEAPGNMGLFDQQLALQWVK 180
QY 181 NIAAFGCGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
Db 181 NIAAFGCGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEAR 240
QY 241 NRTNLAKLTGCSRENETEIIKCLRNKDPQOEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
Db 241 NRTNLAKLTGCSRENETEIIKCLRNKDPQOEILLNEAFVVPYGTPLSVNFGPTVDGDFLT 300
QY 301 DMPDILILELQKQKTOILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFQSGLKIFPPG 360
Db 301 DMPDILILELQKQKTOILVGNKDEGTWFLVYGAPGFSKDNNSIITRKEFQSGLKIFPPG 360
QY 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDYFNFCPALEFTKFSSEGNNAFFYY 420
Db 361 VSEFGKESILFHYTDWDDQRPENYREALGDVVDYFNFCPALEFTKFSSEGNNAFFYY 420
QY 421 FEHRSSKLPWPPEWGMVHGIEFVFGFLPERRDNYTKAEIILSRISIVKRWANFAKYGNP 480
Db 421 FEHRSSKLPWPPEWGMVHGIEFVFGFLPERRDNYTKAEIILSRISIVKRWANFAKYGNP 480
```

Qy 481 NETQNNSTSWPVKSTEOXYLTLTNTESTRIMTKLRAQOCRFWTSFFPKVLEMTGNIDEAE 540
Db 481 NETQNNSTSWPVKSTEOXYLTLTNTESTRIMTKLRAQOCRFWTSFFPKVLEMTGNIDEAE 540
Qy 541 WEWKAGFHRWNNYMDWKNQFNDYTSKKESCVGL 574
Db 541 WEWKAGFHRWNNYMDWKNQFNDYTSKKESCVGL 574

Search completed: July 8, 2005, 11:12:36
Job time : 80 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2005, 11:11:07 ; Search time 71 Seconds
(without alignments)
4139.908 Million cell updates/sec

Title: US-09-748-739a-2_COPY_29_602

Perfect score: 3110

Sequence: 1 EDIIIAIKNGKVRGNLTV.....MDWKQFNIDYTSKESCVGL 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	ID	Description
1	3096	99.5	602	1 CHLE_HUMAN	P06276 homo sapien
2	2843	91.4	581	1 CHLE_RABIT	P21927 oryctolagus
3	2775	89.2	602	2 Q9N1N9	P81908 equus caball
4	2774	89.2	574	1 CHLE_HORSE	P81908 equus caball
5	2696	86.7	602	1 CHLE_FELCA	P02760 felis silve
6	2684	86.3	602	1 CHLE_PANTT	P02761 panthera ti
7	2321	81.1	603	1 CHLE_MOUSE	Q03311 mus musculu
8	2505	80.5	597	2 Q9UKC1	P09341 rattus norv
9	2289	73.6	603	2 Q90ZK8	P09348 gallus gall
10	1765.5	56.8	634	1 ACES_BRARE	Q90ZK8 gallus gall
11	1765	56.8	633	1 ACES_ELEEL	Q42275 electrophor
12	1722.5	55.4	606	1 ACES_BUNFA	Q92035 bungarus fa
13	1691	54.4	614	2 Q67BC1	P67bc1 macaca mula
14	1689	54.3	614	1 ACES_HUMAN	P22303 homo sapien
15	1678.5	54.0	614	1 ACES_RAT	P37136 rattus norv
16	1675.5	53.9	614	1 ACES_MOUSE	P21836 mus musculu
17	1674	53.8	349	2 Q9GKJ6	Q9GKJ6 sus scrofa
18	1666.5	53.6	611	1 ACES_FELCA	P02763 felis silve
19	1663.5	53.5	613	1 ACES_BOVIN	P23795 bos taurus
20	1649.5	53.0	584	1 ACES_RABIT	Q29499 oryctolagus
21	1649	53.0	590	1 ACES_TORMA	P07692 torpedo mar
22	1648	53.0	586	1 ACES_TORCA	P04058 torpedo cal
23	1559.5	50.1	617	2 Q67BC2	P067bc2 macaca mula
24	1557.5	50.1	617	2 Q85TM9	Q85tm9 homo sapien
25	1455.5	46.8	767	1 ACES_CHICK	P36196 gallus gall
26	1435	46.1	602	2 Q76999	P07699 branchiost
27	1376	44.2	605	2 Q76998	P07698 branchiost
28	1358	43.7	526	2 Q86YX9	Q86yx9 homo sapien
29	1323	42.5	701	2 Q75VX9	Q75vx9 cullex trita
30	1319	42.4	702	2 Q6A2E2	Q6a2e2 aedes aegypt
31	1317	42.3	702	1 ACES_CULPI	Q86gc8 cullex pipie

32	1302	41.9	623	2 Q7RTM0	Q7rtm0 anopheles g
33	1302	41.9	737	1 ACB1_ANOGA	Q869c3 anopheles g
34	1302	41.9	743	2 Q7PUR2	Q7pur2 anopheles g
35	1294	41.6	559	2 Q7PKM1	Q7pkm1 anopheles g
36	1273	40.9	687	2 Q86CZ4	Q86cz4 tetranychus
37	1220	39.2	676	2 Q9BMJ1	Q9bmj1 schizaphis
38	1217	39.1	676	2 Q85Z60	Q85z60 aphid gossy
39	1216	39.1	660	2 Q6KAV3	Q6kav3 aphid gossy
40	1214	39.0	676	2 Q65Z63	Q65z63 aphid gossy
41	1213	39.0	671	2 Q6KAV4	Q6kav4 aphid gossy
42	1212	39.0	676	2 Q8MV35	Q8mv35 aphid gossy
43	1209	38.9	675	2 Q6KAV5	Q6kav5 aphid gossy
44	1209	38.9	676	2 Q65Z62	Q65z62 aphid gossy
45	1203	38.7	676	2 Q6BCH8	Q6bch8 rhopalosiph

ALIGNMENTS

RESULT 1

CHLE_HUMAN

ID CHLE_HUMAN STANDARD; PRT; 602 AA.

AC P06276;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)

DE (Choline esterase II) (Butyrylcholine esterase)

DE (pseudocholinesterase)

GN Name=BCHE; Synonyms=CHE1;

OS Homo sapiens (Human);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90212557; PubMed=2322535;

RA Arpagaus M., Kott M., Vatsis K.P., Bartels C.F., la Du B.N.,

RA Lockridge O.;

RT "Structure of the gene for human butyrylcholinesterase. Evidence for a

RT single copy.";

RL Biochemistry 29:124-131(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX TISSUE=Fetal;

RC MEDLINE=87231856; PubMed=3035536;

RA Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O., Soreq H.;

RA "Isolation and characterization of full-length cDNA clones coding for

RA cholinesterase from fetal human tissues.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=88016155; PubMed=3477799;

RA McTierman C., Adkins S., Chatonnet A., Vaughan T.A., Bartels C.F.,

RA Kott M., Rosenberry T.L., la Du B.N., Lockridge O.;

RA "Brain cDNA clone for human cholinesterase.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Skin;

RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Roha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Db	429	EHRSKLPWPBWGMVHGYEIEFVGLPLERRVNYTKAEIILSRISIMKRWANFAKYGNPN	488
Qy	482	ETQNNSTWVPFKSTEQKYLTLNTESPRIMTKLRAQQCRFWTSFPFKVLEMTGNIDEAEW	541
Db	489	GTQNNSTWVPFKSTEQKYLTLNTESPRIMTKLRAQQCRFWTSFPFKVLEMTGNIDEABQ	548
Qy	542	EWKAGFHRWNNYMDWKNFNDYTSKKESC	573
Db	549	EWKAGFHRWNNYMDWKNFNDYTSKKESC	580
RESULT 3			
Q9NIN9	PRELIMINARY; PRT; 602 AA.		
AC	Q9NIN9		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Butyrylcholinesterase (EC 3.1.1.8).		
GN	Name=BCE;		
OS	Equus caballus (Horse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.		
OX	NCBI_TaxID=9796;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=20181263; PubMed=10718335; DOI=10.1016/S0006-2952(99)00389-5;		
RA	Wierdl M., Morton C.L., Danks M.K., Potter P.M.;		
RT	"Isolation and characterization of a cDNA encoding a horse liver		
RT	butyrylcholinesterase: evidence for CPT-11 drug activation.";		
RL	Biochem. Pharmacol. 59:773-781(2000).		
CC	-1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.		
DR	EMBL; AF178685; AAF61480.1; -.		
DR	HSP; P06276; IPOP.		
DR	GO; GO:0004104; F:cholinesterase activity; IEA.		
DR	GO; GO:0016787; F:hydrolyase activity; IEA.		
DR	InterPro; IPR002018; CarbesteraseB.		
DR	InterPro; IPR000997; Cholinesterase.		
DR	InterPro; IPR000379; Ser_estrs.		
DR	Pfam; PF00135; Coesterase; 1.		
DR	PRINTS; PR00878; CHOLNESTRASE.		
DR	PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.		
DR	PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.		
KW	Hydrolase.		
SQ	SEQUENCE. 602 AA; 68938 MW; 94C73F00431DF26E CRC64;		
Query Match 89.2%; Score 2775; DB 2; Length 602;			
Best Local Similarity 90.7%; Pred. No. 2.9e-200;			
Matches 518; Conservative 19; Mismatches 34; Indels 0; Gaps 0;			
Qy	1	EDDIIATKNGKVRGMNLTVFGGTVAFLGIPYAQPPLGRLRFKKQSLTKWSIWNATK	60
Db	29	EEDIIITTKNGKVRGMNLTVFGGTVAFLGIPYAQPPLGRLRFKKQSLTKWSIWNATK	88
Qy	61	YANSCQNIIDQSFPGFHGSEMNPNTLSDECLYNVWIPAKPKNATVLIWYGGGFQT	120
Db	89	YANSCYQNTDQSFPGFHGSEMNPNTLSDECLYNVWIPAKPKNATVLIWYGGGFQT	148
Qy	121	GTSSLHVYDGKFLARVERVIVSMYRVGALGFALPGNPAQNGMFLDQQLALQWVQK	180
Db	149	GTSSLVYDYGKFLARVERVIVSMYRVGALGFALPGNPAQNGMFLDQQLALQWVQK	208
Qy	181	NIAAFGNPKSVTLFGESAGASVSLHLLSPGSHLFTAILQSGSNAPWAVTSLYEAR	240
Db	209	NIAAFGNPKSVTLFGESAGASVSLHLLSPGSHLFTAILQSGSNAPWAVTSLYEAR	268
Qy	241	NRTNLAKLTCGSRNENETIICLRNKPQILLNEAFVVPYGPPLSVNFGPTVDGDFLT	300
Db	269	NRTNLAKLTCGSRNENETIICLRNKPQILLNEAFVVPYGPPLSVNFGPTVDGDFLT	328
Qy	301	DMPDILLBELGQFKTKIILVGNKDEGTWFLVYGPAGFSKDNNSIITRKEFOEGLKIFPPG	360
Db	329	DMPDILLBELGQFKTKIILVGNKDEGTWFLVYGPAGFSKDNNSIITRKEFOEGLKIFPPR	388

```
FT CARBOHYD 486 486 N-linked (GlcNAc...).
SQ SEQUENCE 574 AA; 65641 MW; 07755EB9FB9CB33E CRC64;

Query Match
Best Local Similarity 89.2%; Score 2774; DB 1; Length 574;
Matches 517; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFGTGTATFLGIPYAPPLGLRFRFKKPSQSLTKWSDIWNATK 60
DB 1 EDDIIATKNGKVRGMNLTVFGTGTATFLGIPYAPPLGLRFRFKKPSQSLTKWSDIWNATK 60

QY 61 YANSCQNIDQSPFGFHGSEMNPTDISEDCLYLNVMIPAPKPNATVLIWIYGGGQOT 120
DB 61 YANSCQNIDQSPFGFHGSEMNPTDISEDCLYLNVMIPAPKPNATVLIWIYGGGQOT 120

QY 121 GTSSLHVVDGKFLARVERIVVSMYRVGALGFALPGNPEAPGNMGLFDQQLALQWYOK 180
DB 121 GTSSLHVVDGKFLARVERIVVSMYRVGALGFALPGNPEAPGNMGLFDQQLALQWYOK 180

QY 181 NIAAFGPNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPAVTSLYEAR 240
DB 181 NIAAFGPNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPAVTSLYEAR 240

QY 241 NRTLNKLAKTCCSRENETEIIKLRNKPQOBIILNEAFVVPYGTPLSVNFGTVDGDFLT 300
DB 241 NRTLNKLAKTCCSRENETEIIKLRNKPQOBIILNEAFVVPYGTPLSVNFGTVDGDFLT 300

QY 301 DMPDILLEGQPKTKQIILGVNKGDTWFLVVGAPGFSKDNNSIITRKEFQEGKIFPPG 360
DB 301 DMPDILLEGQPKTKQIILGVNKGDTWFLVVGAPGFSKDNNSIITRKEFQEGKIFPPG 360

QY 361 VSEFGKESILFHYTDWDQDQRPENTREALGDVVDYNTFCPALETKKFSEGNNAFFY 420
DB 361 VSEFGKESILFHYTDWDQDQRPENTREALGDVVDYNTFCPALETKKFSEGNNAFFY 420

QY 421 PEHRSKLPWPBMGMVHGHEIEFVGLPLERRDNYTKAEETLSISIVKRWANFAKYNP 480
DB 421 PEHRSKLPWPBMGMVHGHEIEFVGLPLERRDNYTKAEETLSISIVKRWANFAKYNP 480

QY 481 NETQNNSTWVPFKTEQKYTLNTSTRTIMTKLAQOCRFWTSFPFKVLEMTGNIDBAE 540
DB 481 NETQNNSTWVPFKTEQKYTLNTSTRTIMTKLAQOCRFWTSFPFKVLEMTGNIDBAE 540

QY 541 NEWKAGFHRNNYMDWKNQFNNDYTSKKESC 571
DB 541 NEWKAGFHRNNYMDWKNQFNNDYTSKKESC 571
```

```
RESULT 5
CHLE FELCA STANDARD; PRT; 602 AA.
ID CHLE FELCA
AC O62760;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE (Choline esterase II) (Butyrylcholine esterase)
DE (Pseudocholinesterase).
GN Name=BCE;
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=20334351; PubMed=10874122; DOI=10.1016/S0006-2952(00)00365-8;
RA Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RA Lockridge O.;
RT "Determination of the DNA sequences of acetylcholinesterase and
RT butyrylcholinesterase from cat and demonstration of the existence of
RT both in cat plasma.";
RL Biochem. Pharmacol. 60:479-487(2000).
```

```
CC -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC carboxylic acid anion.
CC -!- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC two subunits in a dimer are linked by a disulfide bond (By
CC similarity).
CC -!- MISCELLANEOUS: Cholinesterase is highly reactive with
CC organophosphate esters (By similarity).
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF053493; AAC06261.1; -.
CC HSP; P22303; I841.
CC InterPro; IPR002018; CarboxylesteraseB.
CC InterPro; IPR000997; Cholinesterase.
CC InterPro; IPR000379; Ser esters.
CC Pfam; PF00135; Coesterase; 1.
CC PRINTS; PR00878; CHOLINESTRASE.
CC PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC Glycoprotein; Hydrolase; Serine esterase; Signal.
CC SIGNAL 1 28
CC CHAIN 29 602
CC ACT_SITE 226 226
CC ACT_SITE 353 353
CC ACT_SITE 466 466
CC DISULFID 93 120
CC DISULFID 280 291
CC DISULFID 428 547
CC DISULFID 599 599
CC CARBOHYD 85 85
CC CARBOHYD 134 134
CC CARBOHYD 269 269
CC CARBOHYD 284 284
CC CARBOHYD 369 369
CC CARBOHYD 483 483
CC CARBOHYD 509 509
CC CARBOHYD 513 513
CC CARBOHYD 514 514
CC SEQUENCE 602 AA; 68328 MW; ECB8879232B74B9C CRC64;

Query Match 86.7%; Score 2696; DB 1; Length 602;
Best Local Similarity 87.6%; Pred. No. 2.6e-194;
Matches 503; Conservative 22; Mismatches 49; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVFGTGTATFLGIPYAPPLGLRFRFKKPSQSLTKWSDIWNATK 60
DB 29 EDDIIATKNGKVRGMNLTVFGTGTATFLGIPYAPPLGLRFRFKKPSQSLTKWSDIWNATK 88

QY 61 YANSCQNIDQSPFGFHGSEMNPTDISEDCLYLNVMIPAPKPNATVLIWIYGGGQOT 120
DB 89 YANSCQNADQSPFGFHGSEMNPTDISEDCLYLNVMIPAPKPNATVLIWIYGGGQOT 148

QY 121 GTSSLHVVDGKFLARVERIVVSMYRVGALGFALPGNPEAPGNMGLFDQQLALQWYOK 180
DB 149 GTSSLHVVDGKFLARVERIVVSMYRVGALGFALPGNPEAPGNMGLFDQQLALQWYOK 208

QY 181 NIAAFGPNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPAVTSLYEAR 240
DB 209 NIAAFGPNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPAVTSLYEAR 268

QY 241 NRTLNKLAKTCCSRENETEIIKLRNKPQOBIILNEAFVVPYGTPLSVNFGTVDGDFLT 300
DB 269 NRTLNKLAKTCCSRENETEIIKLRNKPQOBIILNEAFVVPYGTPLSVNFGTVDGDFLT 328

QY 301 DMPDILLEGQPKTKQIILGVNKGDTWFLVVGAPGFSKDNNSIITRKEFQEGKIFPPG 360
DB 301 DMPDILLEGQPKTKQIILGVNKGDTWFLVVGAPGFSKDNNSIITRKEFQEGKIFPPG 360
```



```
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 597 AA; 67776 MW; 771204D166C7EEAC CRC64;

Query Match
Best Local Similarity 80.5%; Score 2505; DB 2; Length 597;
Matches 458; Conservative 47; Mismatches 69; Indels 0; Gaps 0;

QY 1 EDDIIATKNGKVRGMNLTVPFGTVPFLGIPYAPQPLGLRLRFKKPQSLTKWSDIWNATK 60
DB 24 EEDVIIITKTGRVGLSPILGIGTVPFLGIPYAPQPLGLSLRFRKKPQPLNKPDPVYNATK 83

QY 61 YANSCQNIIDOSFGEHSGEMNNTDISEDCLYLNWIPAPKPNATVLIWYGGGFOT 120
DB 84 YANSCYQNIIDQAFPGFQSEMNNTDISEDCLYLNWIPVPKPNATVMVWYGGGFOT 143

QY 121 GTSSLHVYDGFKLARVERVIVVSMYRVGALGFLALPCNPEAPGNMGLFDQOLALQWVK 180
DB 144 GTSSLPVYDGFKLARVERVIVVSMYRVGALGFLAFPCNSEAPGNMGLFDQOLALQWVK 203

QY 181 NIAAFGNPKSVTLFGESAGAASVSLHLLSPGSHLFTTRAILQSGSNAPWAVTSLYEAR 240
DB 204 NIAAFGNPKSVTLFGESAGAASVSLHLLCPQSYPLFTTRAILQSGSNAPWAVKHPBEAR 263

QY 241 NRTLNKLTCGSRNETEIIKCLRNKDPOBILNEAFVVPYGPPLSVNFGPTVDGDLT 300
DB 264 NRTLTAKFICGSENEKEBIIICLRSKDPOBILNEKVLVPSDSIRSNFGPTVDGDLT 323

QY 301 DMPDILLBLGFKTKTQILVGNKDEGTWFLVYGAPGFSKONNSIITRKEFOEGLKIFPPG 360
DB 324 DMPHTLLQLGKVKTAQLVGNKDEGTAFVYGAPGFSKONDSIITRKEFOEGLNMYFPG 383

QY 361 VSEFGKESILPHYTDVDDQRPENYREALGVGDYNPICPALEFTKFSWGNNAFFYY 420
DB 384 VSSLGKEAILFYVDWLQDTPVYVREAFDIIIGDYNIIICPALEFTKFAELEINAFYY 443

QY 421 FEHRSKLPWPEWGMVHGHEIEFVGLPLERRDNYTKAEIILRSIVKRWANFAKYNP 480
DB 444 FEHRSKLPWPEWGMVHGHEIEFVGLPLERRVNYTRAEIIFRSIMKTWANFAKYGHP 503

QY 481 NETQNNSTWPFVFKSTEOKYLTLTNTESTIMTKLRAQOCRFWTSPFPKVLMTGNIDEAE 540
DB 504 NGTQGNSTWPFVFTSTEOKYLTLTNTEKSKINSKLRAPOCQWRIFFPKVLITGDIIDERE 563

QY 541 WEWAGFHRWNNYMDWKNQNDYTSKKESCVGL 574
DB 564 QEWKAGFHRWNNYMDWKNQNDYTSKKETCTDL 597

RESULT 9
Q90ZK8 ID Q90ZK8 PRELIMINARY; PRT; 603 AA.
AC Q90ZK8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Butyrylcholinesterase precursor (EC 3.1.1.8).
GN Name=BCE;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Geisler K., Chatonnet A., Layer P.G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR EMBL; AJ306928; CAC37792.1; -.
DR HSP; P06276; 1P01.
DR GO; GO:0004104; F:cholinesterase activity; IEA.

DR GO; GO:0016787; F:hydrolase activity; IEA.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Signal.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 603 butyrylcholinesterase.
SQ SEQUENCE 603 AA; 68480 MW; A350PDDP68574ADF CRC64;

Query Match
Best Local Similarity 73.6%; Score 2289; DB 2; Length 603;
Matches 414; Conservative 70; Mismatches 88; Indels 0; Gaps 0;

QY 2 DDIIATKNGKVRGMNLTVPFGTVPFLGIPYAPQPLGLRLRFKKPQSLTKWSDIWNATKY 61
DB 30 EDNVITTEKRGVRGNTLQVLGGTVPFLGIPYKPPIGRLRFKPEPFKWSGIWKATKH 89

QY 62 ANSCQNIIDOSFGEHSGEMNNTDISEDCLYLNWIPAPKPNATVLIWYGGGFOTG 121
DB 90 ANSCYQLIDITYPGFPGTEMNPKTNLSEDCLYLNWIPSPKPNATVMVWYGGSFETG 149

QY 122 TSSLHVYDGFKLARVERVIVVSMYRVGALGFLALPCNPEAPGNMGLFDQOLALQWVK 181
DB 150 STSLPVYDGFKLARVERVIVVSMYRTGALGFLALPCNKEVPNGNAGLFDQOLALQWQEN 209

QY 182 IAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHLFTTRAILQSGSNAPWAVTSLYEAR 241
DB 210 IASFGGNPKSVTLFGESAGASVSYHILSPKSHPLFTRAIQSGSANAPWAAITASEARR 269

QY 242 RTLNKLKTCGSRNETEIIKCLRNKDPOBILNEAFVVPYGPPLSVNFGPTVDGDLT 301
DB 270 RTVALAKQLACPTSDTELICLQDKDPKDIENEVYVVKYFSLLHIYFCPTVDGDLAD 329

QY 302 MPDILLBLGFKTKTQILVGNKDEGTWFLVYGAPGFSKONNSIITRKEFOEGLKIFPPGV 361
DB 330 MPEALIKNGIFKQTQVLVGNKDEGTSFLVYGVGFSKSDSLINKTQFVALTSLSPQV 389

QY 362 SEFGKESILPHYTDVDDQRPENYREALGVGDYNPICPALEFTKFSWGNNAFFYY 421
DB 390 SKLAIESIIIFYTDWNEQKPEHYRDMDVDVIGDHIICPAVEFAKTIAEVGNVFFYFF 449

QY 422 EHRSSKLPWPEWGMVHGHEIEFVGLPLERRDNYTKAEIILRSIVKRWANFAKYNPN 481
DB 450 EHRSSKLPWPEWGMVHGHEIEFVGLPLERRVNYTKAEIILRSMLRYWASFAKTGNPN 509

QY 482 ETQNNSTWPFVFKSTEOKYLTLTNTESTIMTKLRAQOCRFWTSPFPKVLMTGNIDEAE 541
DB 510 GTLINGTRWFVFTSTEOKYLTLTNDAEILTKLRAQOCRFWMNFFFPKVLMTGNIDEAE 569

QY 542 EWKAGFHRWNNYMDWKNQNDYTSKKESCVG 573
DB 570 EWKAGFHRWNNYMDWKNQNDYTSKKERCAG 601

RESULT 10
ACES BRARE
ID ACES BRARE STANDARD; PRT; 634 AA.
AC Q9DDE3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHe).
GN Name=ache;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20576389; PubMed=11016933; DOI=10.1074/jbc.M006308200;
RA Bertrand C., Chatonnet A., Takke C., Yan Y., Postlethwait J.,
```


FT SIGNAL 1 28 Potential.
 FT CHAIN 29 606 Acetylcholinesterase.
 FT ACT SITE 231 606 Acyl-ester intermediate (By similarity).
 FT ACT SITE 338 358 Charge relay system (By similarity).
 FT ACT SITE 471 471 Charge relay system (By similarity).
 FT DISULFID 98 125 By similarity.
 FT DISULFID 285 296 By similarity.
 FT DISULFID 433 522 By similarity.
 FT DISULFID 603 603 Interchain (in isoform T) (By similarity).
 FT CARBOHYD 289 289 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 484 484 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 564 564 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 567 606 DNIEAERQWLEFLHWSAYMMHWKQDFHYNKQRCSEL
 FT -> VDPADRERRGARA (in isoform S).
 FT MUTAGEN 101 101 M->Y: Increases peripheral site ligand binding.
 FT MUTAGEN 316 316 K->D: Increases peripheral site ligand binding.
 FT CONFLICT 268 268 T -> S (in Ref. 3).
 FT CONFLICT 350 350 V -> L (in Ref. 3).
 FT SEQUENCE 606 AA; 68074 MW; B95998AEAE0E5709 CRC64;
 Query Match 55.4%; Score 1722.5; DB 1; Length 606;
 Best Local Similarity 52.9%; Pred. No. 5.5e-121;
 Matches 301; Conservative 110; Mismatches 157; Indels 1; Gaps 1;

QY 3 DIIATKNGKVRGMNLTVEGGTVTAFLGIPYAPQPLGLRLPKKQSLTKWSDIMNATKYA 62
 DB 36 ELKVSQTGTSVGLSLVDGHVSAPLGLIPFAEPPLGRMRFLRPPVPMQHVLDATYK 95
 QY 63 NSCCNQIDQSPFGHSGEMNPNTDLSDECLYNVWIPAPKPKNATVLIWYGGGFGTGT 122
 DB 96 PACYQWDTSYFGQTEWNNRGNSEDCLYLNIVSPSPKDPVLVWYGGGFYSGA 155
 QY 123 SSLHYVDGKFLARVERVIVVMNRYVGAFLGFLALPGNPEAPGNMGLFDQQLALQWVQNI 182
 DB 156 ASLDVYDGRFLTYQNVILVSLSYRGAFLGLPGSPAPGNMGLLDQRLALQWVQNI 215
 QY 183 AAFGNGPKSVTLFGESAGASVLSHLSFGSHSLFTRAILQSGSNAPNATVSLYEARNR 242
 DB 216 HPFGGNPRAVTVFGESAGASVGMHLLSTQSRFLQRAILOGGGNAPNATVTPAESRGR 275
 QY 243 TLNLAKLTGCSRENTEIHKLRNKDQPEILNLEAFVVPYGTPLSVNFGPTVDGDFLTD 302
 DB 276 AALLGKQLGCHFNNSSELVSLRKNPQELIDEESVLPYKSI PRFPVPVVDIGDFPDT 335
 QY 303 PDILLELGQFKTKQILVGNKDEGTWFLVYGAPGSKNNSTIITRKEFOGLKIFPPGVS 362
 DB 336 PEAMLSNGNFKETQVLLGVVKGDEGSYFLTYGLPGFSKONESLISRADFLEGVMSVPHAN 395
 QY 363 EPGKESILPHYTDWDDQRPENYREALGVNCDYNFICPALEFTKFSWGNNAFYYPE 422
 DB 396 DIATADVLQVLDQDQDQDREKREKREKREKREKREKREKREKREKREKREKREKREK 455
 QY 423 HRSSKLPPEWNGVMHGYEIEFVGLPLERRRDNNTKABEILRSIVKRWANFAKYNPNE 482
 DB 456 HRASNLAPPNGVPHGYEIEFVGLPLNDLSNTPQEKELSRMRMYANFARTGNPTD 515
 QY 483 TQNNSTSWPVFKSTQKYLTLNTESTRIMTKLRAQOCRPWTSFFPKVLEMTGNIDEAEWE 542
 DB 516 PADKSGAMPYTTASQPVQVQLNTQPLATQPSLRAQICAFWNHFLPKLLNATNDIEAEARQ 575
 QY 543 WKAGHRNNYMDKQNFNDYTSKKESC 571
 DB 576 WKLEFLHWSAYMMHWKQDFHY-NKQDRC 603

RESULT 13

Q67BC1

ID Q67BC1 PRELIMINARY; PRT; 614 AA.

AC Q67BC1:
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Acetylcholinesterase T-form.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OC NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cohen O., Kronman C., Velan B., Shafferman A.;
 RL "Macaca mulatta acetylcholinesterase gene."
 DE Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR EMBL; AY372522; AAR24295.1; JOINED.
 DR EMBL; AY372523; AAR24295.1; JOINED.
 DR EMBL; AY372526; AAR24295.1; JOINED.
 DR EMBL; AY372524; AAR24295.1; JOINED.
 DR InterPro; IPR002018; Carboxylesterase.
 DR InterPro; IPR000997; Cholinesterase.
 DR InterPro; IPR000379; Ser esters.
 DR Pfam; PF00135; Coesterase; 1.
 DR PRINTS; PR00878; CHOLINESTRASE.
 DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
 SQ SEQUENCE 614 AA; 67772 MW; 7A4FCEE096015C5C CRC64;

Query Match 54.4%; Score 1691; DB 2; Length 614;
 Best Local Similarity 53.0%; Pred. No. 1.3e-118;
 Matches 308; Conservative 102; Mismatches 163; Indels 8; Gaps 5;

QY 1 ED-DIIATKNGKVRGMNLTVEGGTVTAFLGIPYAPQPLGLRLPKKQSLTKWSDIMNAT 59
 DB 35 EDALLTVTRGRLRGIRLTKTPGGPVSAFLGIPFAEPPTGRRFLPPEPKQPMWSGV DAT 94
 QY 60 KYANSCCNIDQSPFGHSGEMNPNTDLSDECLYNVWIPAPKPKNAT-VLIWYGGGF 118
 DB 95 TFQSVCYQVDTLYPGPEGTEWNNRGNSEDCLYLNIVWTPYPRPTSPVWYGGGF 154
 QY 119 QTGTSLLHYVDGKFLARVERVIVVMNRYVGAFLGFLALPGNPEAPGNMGLFDQQLALQWV 178
 DB 155 YSGASSLDVYDGRFLTYQNVILVSLSYRGAFLGLPGSPAPGNMGLLDQRLALQWV 214
 QY 179 OKNTAAFGNGPKSVTLFGESAGASVLSHLSFGSHSLFTRAILQSGSNAPNATVSLYE 238
 DB 215 QENVAAFGGDFTSVTLFGESAGASVGMHLLSTQSRFLFRAVLQSGAPNGPMTVMGB 274
 QY 239 ARNRTNLAKLTGCSRENTEIHKLRNKDQPEILNLEAFVVPYGTPLSVNFGPTV 294
 DB 275 ARRRATQLAHLVGCPPGGTGGNDTELVAQLTRPAQVLVNNHVLPGQSVFRFSFVPV 334
 QY 295 DGDELTDMPDILLELGQFKTKQILVGNKDEGTWFLVYGAPGSKNNSTIITRKEFOGL 354
 DB 335 DGDELTDMPDILLELGQFKTKQILVGNKDEGTWFLVYGAPGSKNNSTIITRKEFOGL 394
 QY 355 KIFPGVSEFGKESILPHYTDWDDQRPENYREALGVNCDYNFICPALEFTKFSWGN 414
 DB 395 RVGVQVSDLAEEAVLHYTLWLPEDPARREALSDVVDHNVVCPVAQLAGRLAAQGA 454
 QY 415 NAFYFVFEHRSKLPWPPEWNGVMHGYEIEFVGLPLERRRDNNTKABEILRSIVKRWANF 474
 DB 455 RVYAYVFEHRASTLSWPLMVGPHGYEIEFVGLPLERRRDNNTKABEILRSIVKRWANF 514
 QY 475 AKYGNPNETQN-NSTSWPVFKSTQKYLTLNTESTRIMTKLRAQOCRPWTSFFPKVLEMT 533
 DB 515 ARTGDNEPRDPKAPQMPPTTAGAQVYVSLDLRLPLEVRGLRAQACAFWNRFLPKLSAT 574
 QY 534 GNIDEAEWEWKAGHRNNYMDKQNFNDYTSKKESC 571
 DB 575 DTLEAEARQWKAERHWSYMMHWKQDFHY-SKQDRCSDL 614

RESULT 14
ACCS_HUMAN STANDARD; PRT; 614 AA.
ID P22303; Q16169; Q9BXP7;
AC 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
GN Name=ACHE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91088577; PubMed=2263619;
RA Soreq H., Ben-Aziz R., Prody C.A., Seidman S., Gnat A., Neville L.,
RA Lieman-Hurwitz J., Lev-Lehman E., Ginzberg D., Lipidot-Lifson Y.,
RA Zakut H.;
RT "Molecular cloning and construction of the coding region for human
RT acetylcholinesterase reveals a G + C-rich attenuating structure.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9688-9692(1990).
RN [2]
RP SEQUENCE OF 521-614 FROM N.A.
RX MEDLINE=21138439; PubMed=11239002; DOI=10.1093/nar/29.6.1352;
RA Wilson M.D., Riener C., Martindale D.W., Schnupf P., Boright A.P.,
RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA Miller W., Koop B.F.;
RT "Comparative analysis of the gene-dense ACHE/TPR2 region on human
RT chromosome 7q22 with the orthologous region on mouse chromosome 5";
RL Nucleic Acids Res. 29:1352-1365(2001).
RN [3]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=94131004; PubMed=8299725; DOI=10.1006/excr.1994.1039;
RA Karpel P., Ben Aziz-Alvora R., Sternfeld M., Ehrlich G., Ginzberg D.,
RA Taroni P., Clementi F., Zakut H., Soreq H.;
RT "Expression of three alternative acetylcholinesterase messenger RNAs
RT in human tumor cell lines of different tissue origins.";
RL Exp. Cell Res. 210:268-277(1994).
RN [4]
RP PARTIAL SEQUENCE.
RC TISSUE=Erythrocyte;
RX MEDLINE=89232136; PubMed=2714437; DOI=10.1016/0014-5793(89)81352-3;
RA Chajlani V., Derr D., Earles B., Schmel E., August T.;
RT "Purification and partial amino acid sequence analysis of human
RT erythrocyte acetylcholinesterase.";
RL FEBS Lett. 247:279-282(1989).
RN [5]
RP MUTAGENESIS OF CYS-611.
RX MEDLINE=92084699; PubMed=1748670;
RA Velan B., Grosfeld H., Kromman C., Leitner M., Gozes Y., Lazar A.,
RA Flashner Y., Marcus D., Cohen S., Shafferman A.;
RT "The effect of elimination of intersubunit disulfide bonds on the
RT activity, assembly, and secretion of recombinant human
RT acetylcholinesterase. Expression of acetylcholinesterase Cys-580-->Ala
RT mutant.";
RL J. Biol. Chem. 266:23977-23984(1991).
RN [6]
RP MUTAGENESIS OF ACTIVE SITE RESIDUES AND OF ASP-206 AND ASP-435.
RX MEDLINE=92388112; PubMed=1517212;
RA Shafferman A., Kromman C., Flashner Y., Leitner M., Grosfeld H.,
RA Ordentlich A., Gozes Y., Cohen S., Ariel N., Barak D.;
RT "Mutagenesis of human acetylcholinesterase. Identification of residues
RT involved in catalytic activity and in polypeptide folding.";
RL J. Biol. Chem. 267:17640-17648(1992).
RN [7]
RP 3D-STRUCTURE MODELING OF 35-574.
RX MEDLINE=98304745; PubMed=9640563;
RA Felder C.E., Botti S.A., Lifson S., Silman I., Sussman J.L.;
RT "External and internal electrostatic potentials of cholinesterase
RT models.";
RL J. Mol. Graph. Model. 15:318-327(1997).

[8]
X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 36-574.
MEDLINE=20508217; PubMed=11053835; DOI=10.1107/S0907444900010659;
Kryger G., Harel M., Giles K., Toker L., Velan B., Lazar A.,
Kronman C., Barak D., Ariel N., Shafferman A., Silman I.,
Sussman J.L.;
"Structures of recombinant native and E202Q mutant human
acetylcholinesterase complexed with the snake-venom toxin fascicul-
in.";
Acta Crystallogr. D 56:1385-1394(2000).
[9]
VARIANT BLOOD GROUP YT(B) ASN-353.
MEDLINE=93256075; PubMed=8488842;
Bartels C.F., Zelinski T., Lockridge O.;
"Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
accounts for yt blood group polymorphism.";
Am. J. Hum. Genet. 52:928-936(1993).
-!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
-!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
-!- SUBUNIT: Homotetramer; composed of disulfide-linked homodimers.
-!- INTERACTS WITH PRIMA1. The interaction with PRIMA1 is required to
anchor it to the basal lamina of cells and organize into tetramers
(by similarity).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=1;
IsoId=P22303-1; Sequence=Displayed;
Name=2;
IsoId=P22303-2; Sequence=VSP_001457;
POLYMORPHISM: ACHE is responsible for the Yt blood group system.
The molecular basis of the Yt(a)=Yt1/Yt(b)=Yt2 blood group
antigens is a single variation in position 353; His-353
corresponds to Yt(a) and the rare variant with Asn-353 to Yt(b).
-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
-!- DATABASE: NAME=Blood group antigen mutation database;
NOTE=Yt blood group system;
WWW="http://www.bloc.aecom.yu.edu/bgmut/Yt.htm".

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

EMBL; M55040; AAA68151.1; -.
EMBL; AF312032; AAK21003.1; -.
EMBL; S71129; AAC60618.1; -.
PIR; A39256; A39256.
PDB; 1B41; X-ray; A=36-574.
PDB; 1F80; X-ray; A=32-614.
PDB; 2CLJ; Model; @=32-574.
SWISS-2DPAGE; P22303; HUMAN.
GeneW; HGNC:108; ACHE.
MIM; 100740; -.
MIM; 112100; -.
GO; GO:0005605; C:basal lamina; NAS.
GO; GO:0005576; C:extracellular; TAS.
GO; GO:0042166; F:acetylcholine binding; NAS.
GO; GO:0003990; F:acetylcholinesterase activity; IMP.
GO; GO:0001540; F:beta-amyloid binding; TAS.
GO; GO:0042803; F:protein homodimerization activity; NAS.
GO; GO:0001507; F:acetylcholine breakdown in synaptic cleft; NAS.
GO; GO:0042982; F:amyloid precursor protein metabolism; TAS.
GO; GO:0007155; P:cell adhesion; TAS.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0006260; P:DNA replication; TAS.
GO; GO:0007517; P:muscle development; TAS.
GO; GO:0050714; P:positive regulation of protein secretion; TAS.
GO; GO:0009611; P:response to wounding; TAS.
GO; GO:0007416; P:synaptogenesis; TAS.

DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLNESTRASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B.1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B.2; 1.
KW 3D-structure; Alternative splicing; Blood group antigen;
KW Direct protein sequencing; Glycoprotein; Hydrolase; Membrane;
KW Neurotransmitter degradation; Polymorphism; Serine esterase; Signal;
KW Synapse.
FT SIGNAL 1 31 Potential.
FT CHAIN 32 614 Acetylcholinesterase.
FT ACT_SITE 234 234 Acyl-ester intermediate.
FT ACT_SITE 365 365 Charge relay system.
FT ACT_SITE 478 478 Charge relay system.
FT DISULFID 100 127
FT DISULFID 298 303
FT DISULFID 440 560
FT DISULFID 611 611 Interchain.
FT CARBOHYD 296 296 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 381 381 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 495 495 N-linked (GlcNAc...) (Potential).
FT VARSPIC 575 614 DTLDEAEQWKAEPHRSYVTHWKNQFDHYSKQDRCSDL
FT FT -> GNGGAGSAGRGVGRQCNPSSLPLASEAPSTCPGFT
FT FT HGEAAPRPGLPLPLLLHQLLLFLSHLRL (in
FT FT isoform 2).
FT FT /FTID=VSP_001457.
FT FT V -> E (in dbSNP:8286).
FT FT /FTID=VAR_011934.
FT FT H -> N (in Yt(b) antigen; dbSNP:1799805).
FT FT /FTID=VAR_002359.
FT FT D -> N: Misfolding, absence of secretion.
FT FT S -> A: Loss of activity.
FT FT E -> A: Loss of activity.
FT FT D -> N: Misfolding, absence of secretion.
FT FT H -> A: Loss of activity.
FT FT C -> A: Impairment of interchain disulfide
FT FT bridge formation.
FT FT
FT TURN 38 39
FT STRAND 40 42
FT STRAND 47 49
FT STRAND 51 53
FT TURN 56 57
FT STRAND 60 67
FT STRAND 69 70
FT STRAND 74 76
FT HELIX 77 78
FT STRAND 82 83
FT STRAND 90 92
FT STRAND 94 94
FT STRAND 99 100
FT TURN 109 110
FT TURN 112 115
FT TURN 116 117
FT STRAND 123 124
FT STRAND 129 135

Query Match 54.3%; Score 1689; DB 1; Length 614;
Best Local Similarity 52.8%; Pred. No. 1.9e-118;
Matches 307; Conservative 104; Mismatches 162; Indels 8; Gaps 5;

QY 1 ED-DIIATKNGKVGMINLVFGGTVTAFLGIPYAPQPLGRURFKKPSQSLTKWSIDWAT 59
DB 35 EDALLTVRGRLGIRLKTGGPVSAFLGIPFAEPMPGPRFLPPPKQPSGVVAT 94
QY 60 KYANSCQNIQDQFPFGHSEMMNPNTDISEDCLYLNWIPAPKPKNAT-VLIWYGGGF 118
DB 95 TFQSVCYQVDTLYPGFEGTEMMNRELSDCLYLNWTPYRPTSPPTPLVWYGGGF 154
QY 119 QGTGSSLVHYDCKFLARVERVIVSMYRVGALGFLALPGNDEAPGNMGLFDQALQWV 178
DB 155 YSGASSLDVYDGRFLVQABRTVLVSMYRVGAFGLFALPGSREAFNGVGLLDQRLQWV 214

QY 179 QKNIAAFGNGPKSVTLFGESAGAAVSUHLHSPQSHSLFTTRAILQSGSFNAPWATVSLYE 238
DB 215 QENVAAGCGDPTSVTLFGESAGAAVSUHLHSPQSHSLFTTRAILQSGSFNAPWATVSGMGE 274
QY 239 ARNRTLNIAKLKTCG----SRENETEIIKCLANKDPOEITLLNEAFVVPVGTPLSVNFGPTV 294
DB 275 ARRTATQAHUHVCGPPGGTGGNDTVELVACLRAQVILVNHVHVLPOESVFRFSFVPV 334
QY 295 DGDFLMDPDIILLEGQFKTKQILVGVNKNDEGTWFLVYGAFCGFKSKDNNSIITRKEFBQGL 354
DB 335 DGDFLSDTPEALINAGDPHGLQVLGVVKGDSYFLVYGAFCGFKSKDNESLISRAEFLAGV 394
QY 355 KIFPPGVSEFGKESILFHYTDWDDQRPENYREALGDVGVNFCPALETKKSEWGN 414
DB 395 RVGPVQNSDLAAEAVALHYTDWLPEDPARLREALSDVGVHNVCPVPAQAGRLAAQGA 454
QY 415 NAFVYFEHRSKLPWPEWGMVMEGYETEFVFGPLERRDDNYTKAEITLSRSIVKRWANF 474
DB 455 RYAYVFEHRASTLSWPLWGMVPHGYETEFVFGPLERRDDNYTKAEITLSRSIVKRWANF 514
QY 475 AKYGNPNETQN-NSTSWPVFKSTQKYLTLNTESTRIMTKLRAQOCQRFWTFFPKVLEMT 533
DB 515 ARTGDPNEPRPKAPQWPPYTAGAQYVSLDLRPLEVRRLRAQACAFNNRFLPKLSAT 574
QY 534 GNIDEAEWEWKAGFHRNNYMMQNPNDYTSKSKSCVGL 574
DB 575 DTLDEAEQWKAEPHRSYVTHWKNQFDHYSKQDRCSDL 614

RESULT 15
ACES_RAT
ID ACES_RAT STANDARD; PRT; 614 AA.
AC P37136;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acetylcholinesterase precursor (EC 3.1.1.7) (ACHE).
GN Name=ACHE;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM T).
RX MEDLINE=93107932; PubMed=8417155;
RA Legay C., Bon S., Vernier P., Coussen F., Massoulié J.;
RT "Cloning and expression of a rat acetylcholinesterase subunit;
RT generation of multiple molecular forms and complementarity with a
RT Torpedo collagenic subunit.";
RL J. Neurochem. 60:337-346(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS H AND R).
RX MEDLINE=93114454; PubMed=8417973; DOI=10.1016/0014-5793(93)81155-S;
RA Legay C., Bon S., Massoulié J.;
RT "Expression of a cDNA encoding the glycolipid-anchored form of rat
RT acetylcholinesterase.";
RL FEBS Lett. 315:163-166(1993).
CC -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -!- SUBUNIT: Homotetramer; composed of disulfide-linked homodimers.
CC Catalytic forms H (GPI-anchor dimer) and T (asymmetric collagen-
CC tailed), which differ in their C-terminus, account for all types
CC of known AChE forms. Interacts with PRIMA1. The interaction with
CC PRIMA1 is required to anchor it to the basal lamina of cells and
CC organize into tetramers (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=T;
CC IsoId=P37136-1; Sequence=Displayed;
CC Name=H;
CC IsoId=P37136-2; Sequence=VSP_001458;
CC Name=R;

```
CC      IsoId=P37136-3; Sequence=VSP_001459;
CC      Note-May be not functional;
CC      -!- TISSUE SPECIFICITY: Has been found in central nervous system and
CC      muscle. Found in embryonic liver and spleen but not in adult
CC      liver.
CC      -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; S50879; AAB24586.1; -
CC      EMBL; X70140; CAA49717.1; -
CC      EMBL; X70141; CAA49718.1; -
CC      PIR; JH0811; JH0811.
CC      HSP; P21836; LMAA.
CC      RGD; 69313; Ache
CC      InterPro; IPR002018; CarboxylesteraseB.
CC      InterPro; IPR000997; Cholinesterase.
CC      InterPro; IPR000379; Ser esters.
CC      Pfam; PF00135; Coesterase; 1.
CC      PRINTS; PR00878; CHOLINESTRASE.
CC      PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC      PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC      Alternative splicing; Glycoprotein; Hydrolase; Membrane;
CC      Neurotransmitter degradation; Serine esterase; Signal; Synapse.
CC      SIGNAL
CC      1      31      Potential.
CC      FT      CHAIN      32      614      Acetylcholinesterase.
CC      FT      ACT_SITE   234      234      Acyl-ester intermediate (By similarity).
CC      FT      ACT_SITE   365      365      Charge relay system (By similarity).
CC      FT      ACT_SITE   478      478      Charge relay system (By similarity).
CC      FT      DISULFID   100      127      By similarity.
CC      FT      DISULFID   288      303      By similarity.
CC      FT      DISULFID   440      560      By similarity.
CC      FT      DISULFID   611      611      Interchain (By similarity).
CC      FT      CARBOHYD    296      296      N-linked (GlcNAc...) (Potential).
CC      FT      CARBOHYD    381      381      N-linked (GlcNAc...) (Potential).
CC      FT      CARBOHYD    495      495      N-linked (GlcNAc...) (Potential).
CC      FT      VARSPPLIC  575      614      DTLDEARQWKAEPHRSYVHWNQDFDHYSKQRCSDL
CC      FT      FTID=VSP_001458.
CC      FT      FTID=VSP_001458.
CC      FT      VARSPPLIC  575      614      DTLDEARQWKAEPHRSYVHWNQDFDHYSKQRCSDL
CC      FT      FTID=VSP_001459.
CC      FT      isoform R.
CC      FT      FTID=VSP_001459.
CC      FT      SEQUENCE  614 AA; 68196 MW; 2EDA7D46282E7C0 CRC64;
```

Search completed: July 8, 2005, 11:13:54
Job time : 75 secs

```
Db      276 RRRATLLARLVGCPGCGAGGNDTELISCLTRPAQDLVDHEWHLVPOESIFRFSFVPVVD 335
Qy      296 GDFLTMPDILLGLGQFKKTOILGVNKGDEGTWFLVYVGAPGSKDNNSIITRKEFOGLK 355
Db      336 GDFLSDTPDALINTGDFQDLQVLGVVVKDEGSYFLVYGVFGSKDNESLISRAQFLAGVR 395
Qy      356 IFPPGVSEFGKESILPHYTDWDDQRPENYREALGDVVDYNFICPALEFTKPFSEWGN 415
Db      396 IGVPQASDLAAEAVVLHYTDLHPEDPAHLRDAMSAVVDHNVVCPVAQLAGRLAAQGAR 455
Qy      416 APFYFHRSSKLPWPPEWGMVHGYEIEFVGLPLERRDNYTKABEILSRISIVKRWANFA 475
Db      456 VYAYIFHRASLTLTWPLWVGVPHGYEIEFVGLPLDPSLNTVVEERIFAQRLMQYWTNFA 515
Qy      476 KYGNPNETQNN-STSWVPVFKSTEQYLTLNTESTRIMTKLRAQOCREWTSPFPKVLMTG 534
Db      516 RTGDPNDPRDSKSPRWPPYTTAAQQYVSLNKLPLEVRERGLRAQTCAFWNRFLPKLSATD 575
Qy      535 NIDEAEWEWKAGFHRNNYMMWMDKNQFNQDNTSKKESCGL 574
Db      576 TLDEARQWKAEPHRSYVHWNQDFDHY-SKQERCSDL 614
```

```
Query Match 54.0%; Score 1678.5; DB 1; Length 614;
Best Local Similarity 53.1%; Pred. No. 1.le-117;
Matches 308; Conservative 102; Mismatches 163; Indels 7; Gaps 4;

Qy      1 EDDIIIAIKNGKVRGMNLTVGTTAEIGIPYAPPLGRLEKFKPSQLTKWSDIWNATK 60
Db      36 DPQLLVVRGGOLGIRLKAPGPPVSAFLGIPFAEPVGRSRFPPEPRPWSGLDATT 95

Qy      61 VANSCCQNDOSFPFGHSGEMNPNPNTLSDCLYNVWIPAPKPKNAT-VLIWIYGGGFQ 119
Db      96 FQNVCYQVDTLYPGFEGTEMNPNRELSDCLYLVNTPYRPTSPTPVLIWIYGGFY 155

Qy      120 TCTSSLHYVDGKFLARVERVIVSNRYRGALGFALPGNPEAPGNMGLFDQQLALQWQ 179
Db      156 SCASSLDVYDGRFLAQVEGTVLVSNRYRGVTFGLFALPGSREAPGNVGLLDQRLALQWQ 215

Qy      180 KNIAAFGNGPKSVTLFGSAGAAVSLLSLPGSHLFTAILQSGSFNAPWAVTSLYE 239
Db      216 ENIAAFGGDPMSVTLFGSAGAAVSVMHLLSLPSRSLFRAVLQSGTNGPWATVAGEA 275

Qy      240 RNRTLNLAKLTGC----SRENETEIKCLRNDKPOEILLNEAFVVPYGTPLSVNFGPTVD 295
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2005, 11:11:07 ; Search time 19 Seconds
(without alignments)
2906.759 Million cell updates/sec

Title: US-09-748-739A-2_COPY_29_602

Perfect score: 3110
Sequence: 1 EDDIIITKNGKVRGNLTV.....MDWKQNFNDYTSKESCVGL 574

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3096	99.5	581	1	ACHU
2	2843	91.4	602	2	cholinesterase (EC
3	2521	81.1	603	2	cholinesterase (EC
4	1785.5	57.4	596	1	acetylcholinesterase
5	1784.5	57.4	599	1	acetylcholinesterase
6	1689	54.3	614	2	acetylcholinesterase
7	1678.5	54.0	614	2	acetylcholinesterase
8	1675.5	53.9	614	2	acetylcholinesterase
9	1639	52.7	584	2	acetylcholinesterase
10	1636.5	52.6	583	2	acetylcholinesterase
11	1455.5	46.8	767	2	acetylcholinesterase
12	1142	36.7	620	2	acetylcholinesterase
13	1070.5	34.4	637	2	acetylcholinesterase
14	1044	33.6	746	2	acetylcholinesterase
15	1040.5	33.5	691	2	acetylcholinesterase
16	1030.5	33.1	664	2	acetylcholinesterase
17	1012.5	32.6	602	2	acetylcholinesterase
18	948	30.5	629	2	acetylcholinesterase
19	937	30.1	584	2	acetylcholinesterase
20	930	29.9	607	2	acetylcholinesterase
21	893	28.7	532	2	acetylcholinesterase
22	754	24.2	532	2	acetylcholinesterase
23	753	24.2	141	2	cholinesterase (EC
24	732	23.5	599	2	sterol esterase (E
25	729	23.4	597	2	sterol esterase (E
26	728.5	23.4	559	1	carboxylesterase (
27	726	23.3	612	2	sterol esterase (E
28	724	23.3	141	2	cholinesterase (EC
29	721	23.2	141	2	cholinesterase (EC

30	721	23.2	141	2	B39768	cholinesterase (EC
31	718.5	23.1	561	2	S47655	carboxylesterase (
32	715	23.0	554	2	A39060	carboxylesterase (
33	711	22.9	745	2	S13586	triacylglycerol li
34	708.5	22.8	565	2	S10367	carboxylesterase (
35	707	22.7	141	2	E39768	cholinesterase (EC
36	701.5	22.6	557	2	A47162	cholinesterase B (E
37	697.5	22.4	567	1	A41010	carboxylesterase (
38	696.5	22.4	562	2	A55281	carboxylesterase (
39	694.5	22.3	561	2	JC2447	carboxylesterase (
40	690.5	22.2	566	2	S19307	carboxylesterase (
41	690	22.2	549	2	JX0054	carboxylesterase (
42	689	22.2	540	2	A31584	carboxylesterase (
43	680.5	21.9	561	2	S62788	carboxylesterase (
44	675.5	21.7	561	2	S71597	carboxylesterase (
45	666	21.4	956	2	A56920	gliotactin precurs

RESULT 1

ACHU

cholinesterase (EC 3.1.1.8) precursor [validated] - human

N:Alternate names: acylcholine acylhydrolase; butyrylcholinesterase; choline esterase II

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004

C:Accession: A33769; A33887; A34668; A00772

R:Arpagaus, M.; Kott, M.; Vatsis, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.

Biochemistry 29, 124-131, 1990

A:Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single cc

A:Reference number: A33769; MUID:90212557; PMID:2322535

A:Accession: A33769

A:Molecule type: DNA

A:Residues: 'MSVQNLQAGAAACISPKYMIPTPKLHLCRESIN', 1-602 <ARP>

A:Cross-references: UNIPROT:P06276; GB:M32391; GB:J02879

A:Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for tra

R:Prody, C.A.; Zevin-Sonkin, D.; Gnatt, A.; Goldberg, O.; Soreq, H.

Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987

A:Title: Isolation and characterization of full-length cDNA clones coding for cholineste

A:Reference number: A26613; MUID:87231856; PMID:3035536

A:Accession: A26613

A:Molecule type: mRNA

A:Residues: 1-133, 'D', 135-602 <PRO>

R:McTernan, C.; Adkins, S.; Chatonnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; Rose

Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987

A:Title: Brain cDNA clone for human cholinesterase.

A:Reference number: A33887; MUID:88016155; PMID:3477799

A:Accession: A33887

A:Molecule type: mRNA

A:Residues: 'MSVQNLQAGAAACISPKYMIPTPKLHLCRESIN', 1-602 <MCT>

A:Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for tra

R:Nogueira, C.P.; McGuire, M.C.; Graesser, C.; Bartels, C.F.; Arpagaus, M.; Van der Spek,

Am. J. Hum. Genet. 46, 934-942, 1990

A:Title: Identification of a frameshift mutation responsible for the silent phenotype of

A:Reference number: A34668; MUID:90252779; PMID:2339692

A:Accession: A34668

A:Molecule type: DNA

A:Residues: 143-145, 'VSNWNIIPTCL', <NOG>

A:Note: frameshift mutant in codon for residue 145 (Gly)

R:Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S.E.; Johnson, L.L.

J. Biol. Chem. 262, 549-557, 1987

A:Title: Complete amino acid sequence of human serum cholinesterase.

A:Reference number: A00772; MUID:87109144; PMID:3542989

A:Accession: A00772

A:Molecule type: protein

A:Residues: 29-602 <LOC>

A:Experimental source: plasma

C:Comment: Cholinesterase is present in most cells (except erythrocytes).

C:Genetics:

A:Gene: GDB:BCHE; CHE1

A:Cross-references: GDB:120558; OMIM:177400

A:Map position: 3q26.1-3q26.2

RESULT 4
ACRYE
N;Alternate names: acetylcholinesterase, asymmetric form
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 17-Mar-1987 #sequence revision 08-Nov-1996 #text change 09-Jul-2004

Qy 295 DGDPLTMDPDLLELGGQFKTKQIILVGVNKGDTWFLVYGAQGFSDKNNSIITRKSEFQEG 355
 Db 335 DGDPLSTPEALINAGDFHGLQVLGVVVKDSEGYPLVYGAQGFSDKNESLISRAEFLAGV 394
 Qy 355 KIRPPGVSEFGKESILFHYTIDWDVDDORPENYREALGDDVGVNFTCPALEFTKKFSEWGN 414
 Db 395 RVGVQVSDDLAAEAVVLHYTDWLHPEDPARLREALSDVVGDRNVVCPVAQLAGRLAAQGA 454
 Qy 415 NAFPPYFEHRSSKLPWPENMGVHGHEYEFVGLPRLERRDNYTKAEELISRSIVKRWANF 474
 Db 455 RVYAYVFEHRASTLSWPLWMCVPHGYEIEFIFGLDPSRNYTAEKIFAQRLMRWYANF 514
 Qy 475 AKYGNPHETQY-NTSPVPVFKSTQKYTLTINTESTRIMTKLRAQOCRFWTSFFPKVLEWT 533
 Db 515 ARTGDNPEDRPDKAPQPPYTAGAQYVSLDRLPLEVRGRGLRAQACAFMNRFLPKLLSAT 574
 Qy 534 GNIDEAEWKKAGFHRNNYMMDKNQFNNDYTSKKESCVCGL 574
 Db 575 DTLDEARQWKAEFHRSSYVHWKYNQDHY-SKQDRCSDL 614

RESULT 7
 JH0811
 acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C/Accession: JH0811
 R/Legay, C.; Bon, S.; Vernier, P.; Coussens, F.; Massoulie, J.
 J. Neurochem. 60, 337-346, 1993
 A/Title: Cloning and expression of a rat acetylcholinesterase subunit: generat
 A/Reference number: JH0811; MUID:93107932; PMID:8417155
 A/Accession: JH0811
 A/Molecule type: mRNA
 A/Residues: 1-614 <LEG>
 A/Cross-references: UNIPROT:P37136; GB:S50879; NID:g262092; PIDN:AAB24586.1; P
 A/Experimental source: striatum
 C/Comment: This protein is responsible for hydrolysis of acetylcholine at chol
 C/Superfamily: cholinesterase; cholinesterase homology
 C/Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle
 F:1-31/Domain: signal sequence #status predicted <SIG>
 F:32-614/Product: acetylcholinesterase catalytic chain #status predicted <MAT>
 F:63-569/Domain: cholinesterase homology <CHE>
 F:100-127,288-303,440-560/Disulfide bonds: #status predicted
 F:234,365,478/Active site: Ser, Glu, His #status predicted
 F:296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.0%; Score 1678.5; DB 2; Length 614;
 Best Local Similarity 53.1%; Pred. No. 1.4e-120;
 Matches 308; Conservative 102; Mismatches 163; Indels 7; Gaps 4

Qy 1 EDDIITATKNGKVRGMNLTVPFGGTVTAPLGHYPYAQPLGLRLRFKFKPSQSLTKWSDIWNATK 60
 Db 36 DPQLLVVRGGQLGRLKAPGPGVSAFLGIPFAEPVGSRRFMEPEPKRPSGILDALT 95
 Qy 61 YANSCQNIQDSFPFGHSEMMNPNTDISEDCLYLNNWIPAPKPKNAT-VLIWIYGGGGFQ 119
 Db 96 FQNVCYQVDTLYPGFEGTEMMNPNNRELSDECLYLNNWTPYPRTPSPVLIWIYGGGFY 155
 Qy 120 TGTSSLVHYDGKFLARVERVIVSNMYRVGALGLFALPGNDEAPGNMGLFDQOLALQWVO 179
 Db 156 SGASSLDVYDGRFLAQVEGTVLVSNNYRVGTFGLFALPGSREAPGNVGLDQRLALQWVO 215
 Qy 180 KNIAAFGNGPKSVTLFGESAGAAVSLSHLSPGSHSLFTRATLQSGSFNAPWAVTSLYEA 239
 Db 216 ENIAAFGDPMSVTLFGESAGAAVSVMHLSPLSRSLFHRVAVLQSGTPNGPWTVSAGEA 275
 Qy 240 RNRTLNLAKTGC---SRENETETIIKLRNKDPOEILLNEAFVVPYGPPLSVNFGPTVD 295
 Db 276 RRRATLLARLVGCPGGAGGNDTELISCLTRPAQDLVDHWHVLPQESSIPRFSFVPPVD 335
 Qy 296 GDFLTMDPDLLELGGQFKTKQIILVGVNKGDTWFLVYGAQGFSDKNNSIITRKSEFQEG 355

```
Db 336 GDFLSDTPDALINTGDFQDLQVLGVVVKDEGSFLVYGVPGFSKDNESSLISRAQFLAGVR 395
Qy 356 IFFPGVSEFGKESILFHYTDMVDQDORPENYREALGDVVGDVNFICPALEFTKKFSEWGN 415
Db 396 IGVPQASDLAAEAUVLHYTDMWHPEDFAHLRDAMSAAVVDHNVVCPVAQLAGRLAAQAGAR 455
Qy 416 AFFYFHRSSKLPWPBWGMVGHGYEIEFFVGLPLERRDNYTKAEELSRISVKKRWANFA 475
Db 456 VYAIYFHRASLTLPWLMGVPHGYEIEFFVGLPLDSLNVTYERIFAQRLMQYWTNFA 515
Qy 476 KYGNPNETQNN-STSWPVFKSTEOKYLTNLNTESTRIMTKLRAQOCRFWTFFPKVLEMTG 534
Db 516 RTGDPNDPRDSKSPWPPTTAAQYVSLNKLPLEVRGLRAQTCAFWNRFLPKLLSATD 575
Qy 535 NIDEAEWKAEGFHRNNYMDWKNQNDYTSKKESCVGL 574
Db 576 TLDEAEQWKAEBFHRSSVMVHWKQFDHY-SKQERCSDL 614

RESULT 8
JH0314
acetylcholinesterase (EC 3.1.1.7) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: JH0314
R:Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.
Neuron 5, 317-327, 1990
A:Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alterna
A:Reference number: JH0314; MUID:90380429; PMID:2400605
A:Accession: JH0314
A:Molecule type: mRNA
A:Residues: 1-614 <RAC>
A:Cross-references: UNIPROT:P21836; EMBL:X56518; NID:G49844; PID:CAA39867.1; PID:G49845
A:Experimental source: brain
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-614/Product: acetylcholinesterase #status predicted <MAT>
F:63-569/Domain: cholinesterase homology <CHE>
F:100-127,288-303,440-560/Diulfide bonds: #status predicted
F:234/Active site: Ser #status predicted
F:296,381,495/Binding site: carbohydate (Asn) (covalent) #status predicted

Query Match 53.9%; Score 1675.5; DB 2; Length 614;
Best Local Similarity 52.8%; Pred. No. 2.4e-120;
Matches 306; Conservative 104; Mismatches 163; Indels 7; Gaps 4;

Qy 1 EDDIIATKNGKVRGMNLTVEGGTVTAFLGIPYAQPPLGLRLRFKPKQSLTKWSDIMNATK 60
Db 36 DPQLLVVRGQLRGIRLKAQPGVSAFLGIPFAEPVGSRRFPPEPKRPWSGVLDATT 95
Qy 61 YANSCCQNIQDOSPPFGHSEMNPNNTDLSDCILYNWIPAPKPKNAT-VLIWYGGGFQ 119
Db 96 FQNVCYQVDTLYPGFEGTEMMNPNRELSDCILYNWTPYPRASPTPVLWYIYGGGFY 155
Qy 120 TGTSSLHYVDGKFLARVERVIVSNRVGALGFALPGNPAQNNGLFPDQALQWVQ 179
Db 156 SGAASLDVYDGRFLAQVEGAVLVSNNRVGTGFLALPGSREAPGNVGLDQRLALQWV 215
Qy 180 KNIAAFGNGPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWATVSLYE 239
Db 216 ENIAAFGDPMSVTLFGESAGAASVGMHLSLPSRSFLHRAVLQSGTPNGPWATVSAGEA 275
Qy 240 RNRTLNAKLTCG----SRENETEIIKLRNKDQEIILNEAFVVPVYGTPLSVNFGPTVD 295
Db 276 RRRATLLARLVGCPGGAGGNDTBLIACLRTPAQDLVDHWHVLPQESIFRFSFVPVVD 335
Qy 296 GDFLTMDPDIILELQGFKKTKTQILVGVNKDEGTWFLVYCAPGFSKDNNSIITRKEFQBLK 355
Db 336 GDFLSDTPDALINTGDFQDLQVLGVVVKDEGSFLVYGVPGFSKDNESSLISRAQFLAGVR 395
Qy 356 IFFPGVSEFGKESILFHYTDMVDQDORPENYREALGDVVGDVNFICPALEFTKKFSEWGN 415
```

```
Db 396 IGVPQASDLAAEAUVLHYTDMWHPEDFTHLRDAMSAAVVDHNVVCPVAQLAGRLAAQAGAR 455
Qy 416 AFFYFHRSSKLPWPBWGMVGHGYEIEFFVGLPLERRDNYTKAEELSRISVKKRWANFA 475
Db 456 VYAIYFHRASLTLPWLMGVPHGYEIEFFVGLPLDSLNVTYERIFAQRLMKYWTNFA 515
Qy 476 KYGNPNETQNN-STSWPVFKSTEOKYLTNLNTESTRIMTKLRAQOCRFWTFFPKVLEMTG 534
Db 516 RTGDPNDPRDSKSPWPPTTAAQYVSLNKLPLEVRGLRAQTCAFWNRFLPKLLSATD 575
Qy 535 NIDEAEWKAEGFHRNNYMDWKNQNDYTSKKESCVGL 574
Db 576 TLDEAEQWKAEBFHRSSVMVHWKQFDHY-SKQERCSDL 614

RESULT 9
S48724
acetylcholinesterase - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 14-Nov-1997
C:Accession: S48724
R:Jbilo, O.; L'Hermite, Y.; Tulesa, V.; Toutant, J.P.; Chatonnet, A.
Eur. J. Biochem. 225, 115-124, 1994
A:Title: Acetylcholinesterase and butyrylcholinesterase expression in adult rabbit tissu
A:Reference number: S48724; MUID:95010096; PMID:7925428
A:Accession: S48724
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-584 <JBI>
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: glycoprotein
F:32-539/Domain: cholinesterase homology <CHE>

Query Match 52.7%; Score 1639; DB 2; Length 584;
Best Local Similarity 51.5%; Pred. No. 1.4e-117;
Matches 299; Conservative 106; Mismatches 168; Indels 8; Gaps 5;

Qy 1 EDDIIATKNGKVRGMNLTVEGGTVTAFLGIPYAQPPLGLRLRFKPKQSLTKWSDIMNATK 60
Db 5 DPQLLVVRGQLRGIRLKAQPGVSAFLGIPFAEPVGSRRFPPEPKRPWSGVLDATA 64
Qy 61 YANSCCQNIQDOSPPFGHSEMNPNNTDLSDCILYNWIPAPKPKNAT-VLIWYGGGFQ 119
Db 65 FQNVCYQVDTLYPGFEGTEMMNPNRELSDCILYNWTPYPRPTSPTPVLWYIYGGGFY 124
Qy 120 TGTSSLHYVDGKFLARVERVIVVSM-NYRVGALGFALPGNPAQNNGLFPDQALQWV 178
Db 125 SGAASLDVYVYGRFLVQAEGTVLVMHNYRVGAFGFTCLPGSREAPGNVGLDQRLALQWV 184
Qy 179 QKNIAAFGNGPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNAPWATVSLYE 238
Db 185 QENVAAFGDPASVTLFGESAGAASVGLHLLSPSRGLFHRAVLQSGAPNGPWATVGVGE 244
Qy 239 ARNRTLNAKLTCG----SRENETEIIKLRNKDQEIILNEAFVVPVYGTPLSVNFGPTV 294
Db 245 ARRRATLLARLVVCPGGAGGNDTELVACLTRPAQDLVDHWRVLPQESIFRFSFVPV 304
Qy 295 DGDFLTMDPDIILELQGFKKTKTQILVGVNKDEGTWFLVYCAPGFSKDNNSIITRKEFQBL 354
Db 305 DGDFLSDTPDALINTGDFQDLQVLGVVVKDEGTWFLVYCAPGFSKDNNEISRAQFLAGV 364
Qy 355 KIFPPGVSEFGKESILFHYTDMVDQDORPENYREALGDVVGDVNFICPALEFTKKFSEWGN 414
Db 365 RVGVQASDLAAEAUVLHYTDMWHPEDPARLDALSVDVGDHNVVCPVAQLAGRLAAQGA 424
Qy 415 NAFYFHRSSKLPWPBWGMVGHGYEIEFFVGLPLERRDNYTKAEELSRISVKKRWANF 474
Db 425 RVYAYVFEHRASTLSWPLWVPHGYEIEFFVGLPLEPSLNTYSEERIFAQRLMYWANF 484
Qy 475 AKYGNPNETQN-NSTSWPVFKSTEOKYLTNLNTESTRIMTKLRAQOCRFWTFFPKVLEMT 533
Db 485 ARTGDPNEPRDAKAPWPPYTAGAQYVSLNKLPLEVRGLRAQACAFWNRFLPKLLSAT 544
```

Qy	534 GNIDAEWEWKAGFHRWNNYMDWNQNFNDYTSSKESCVGL 574 : : : : : : :
Db	545 DTLDEAERQWKAEFHRWSSYVHWKNQFDHY-SKQDRCSDL 584

RESULT 10

S10712
acetylcholinesterase (EC 3.1.1.7) - bovine acetylcholine esterase from Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Nov-1993 #sequence revision 23-Mar-1995 #text_change 12-May-1995
C;Accession: S10712; A39734; B39734; B25650
R;Doctor, B.P.; Chapman, T.C.; Christner, C.E.; Deal, C.D.; de la Hoz, D.M.; Gentry, M.K.
FEBS Lett. 266, 123-127, 1990
A;Title: Complete amino acid sequence of fetal bovine serum acetylcholinesterase and its cDNA
A;Reference number: S10712; MUID:90306335; PMID:2365060
A;Accession: S10712
A;Molecule type: protein
A;Residues: 1-583 <DOC>
A;Experimental source: fetal serum
R;Roberts, W.L.; Doctor, B.P.; Foster, J.D.; Rosenberry, T.L.
J. Biol. Chem. 266, 7481-7487, 1991
A;Title: Bovine brain acetylcholinesterase primary sequence involved in intersubunit disulfide bond formation
A;Reference number: A39734; MUID:91210255; PMID:2019579
A;Accession: A39734
A;Molecule type: protein
A;Residues: 1-15, 'R', 17-38, 225-235, 'X', 237-244, 248-264, 'X', 266-273, 365-380; 396-404, 'X', 405-410
A;Experimental source: brain, erythrocyte
A;Accession: B39734
A;Molecule type: protein
A;Residues: 1-38 <RO2>
A;Experimental source: fetal serum
R;Bon, S.; Chang, J.Y.; Strosberg, A.D.
FEBS Lett. 209, 206-212, 1986
A;Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-soluble forms of acetylcholinesterase
A;Reference number: A91370; MUID:87080761; PMID:3792544
A;Accession: B25650
A;Molecule type: protein
A;Residues: 'XS', 3-12 <BON>
A;Experimental source: caudate nucleus
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
F;32-538/domain: cholinesterase homology <CHE>
F;61,265,350,464,541/Binding site: carbohydrate (asn) (covalent) #status predicted
F;203/Active site: Ser #status predicted

Query Match	52.6%;	Score	1636.5;	DB 2;	Length	583;			
Best Local Similarity	51.7%;	Pred.	No. 2.1e-117;						
Matches	300;	Conservative	103;	Mismatches	170;	Indels	7;	Gaps	4;
Qy	1	EDDIIITATKNGKVRGMNLTIVFGGTYTAFGLIPYAPPLGLRLRRFKKQSLTKWSDIWNATK	60	:	:	:	:	:	:
Db	5	DELLVWVRGGELGRLMAPRGPVSAFLGIPFAEPVPVGRPRFLPPFKRPWPGVLNATA	64	:	:	:	:	:	:
Qy	61	YANSCQNTDQSPFGHSGEMNPNITLSEDCLYLNWIPAPKPKNAT-VLIWYGGGFG	119	:	:	:	:	:	:
Db	65	FQSCVCYQYVDLTLYPCFEGTEGMNPNRELSEDCLYLNWTPVPRSSPTPLVWYGGGFY	124	:	:	:	:	:	:
Qy	120	TGTSSLHVYDQGFKLARVERVIVSNRYVGALGFLALPGNPAPGNMGLFDQOALQWVQ	179	:	:	:	:	:	:
Db	125	SCASSLDVYDGRFLVQAEGTFLVSNRYVGAFGLALPGSREAPGNVGLDDQRLAQSVQ	184	:	:	:	:	:	:
Qy	180	KNTAFEGNPKSVTLPGFSAGAAVSYLHLSPGSHSLFTRAILQSGSFNAPWATSI.YEA	239	:	:	:	:	:	:
Db	185	ENVAAPGGDPTSVTLPGFSAGAAVSVMHLLSPGSGLTFHRAVLQSGAPGNWATVGVGEA	244	:	:	:	:	:	:
Qy	240	RNRITLMLAKITGC- ---SRENETEYIKCLRKNKDQEIILNEAFVVPYGTPLSNVFGPTVD	295	:	:	:	:	:	:
Db	245	RRRATLLARLVGCPGCGAGNDTELVALCLRAPQAQDLVDHEWRVLPQEHVFRFSFVPPVD	304	:	:	:	:	:	:
Qy	296	GFQFLTMDPDIILELGGFKKTIQLIVGVNKDBGTWFLVYAGPGFSKNNNSIITRKEPQGLK	355	:	:	:	:	:	:
Db	305	GFPLSDTPBALINAGDFVGLQVILVGWVKDEGSYFLVYAGPGFSKDNESLLSRAQFLAGVVR	364	:	:	:	:	:	:

```

356 Qy 1FFPGVSEFGKESILFHYTDWDDQRPENYREALGDVVGVNDYNYFICPALEFTKKFSEWGN 415
365 Db VGVQPQSDALAAEAVVLHYTDLWHPEDPARWREALSDVVGDHNVGCPVAQLAGRLAAQGAR 424
416 Qy AFFYFEHRRSSKLPWPEMMGYHGYEIEFVFGPLPLERDNTYKASEILLSRVKAWANFA 475
425 Db VYAIIFERASTLSWPLWMGVPHGYEIEFIFGLPLEPSLNYTIEBRTFAQLRLMYWANFA 484
476 Qy KYGNPNETQ-NNSTSWPVFKSTEQKYLTLNTTESTIMTKLAQQCRFWTSFPFKVLEMTG 534
485 Db RTGDPNDRAPKAPQWPYPYTAGAQYVSLNLRPLGVPQASRAQACAFWNRFLPKLINATD 544
535 Qy NIDAEAEWKKAGFRWNNYMDKWNQFNNDYTSKKESCVCGL 574
545 Db TLDABERQWKAERHWSYIMVHWKNQFDHY-SKQDRCSDL 583

RESULT 11
S47639
acetylcholinesterase (EC 3.1.1.7) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S47639
R:Randall, W.R.; Rimer, M.; Gough, N.R.
Biochim. Biophys. Acta 1218, 453-456, 1994
A:Title: Cloning and analysis of chicken acetylcholinesterase transcripts from
A:Reference number: S47639; MUID:9432359; PMID:8049273
A:Accession: S47639
A:Molecule type: mRNA
A:Residues: 1-767 <RAN>
A:Cross-references: UNIPROT:P36196; EMBL:U03472; NID:G623031; PIDN:AAA60456.1;
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

```

RESULTS

S47639 acetylcholinesterase (EC 3.1.1.7) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S47639
R:Randall, W.R.; Rimer, M.; Gough, N.R.
Biochim. Biophys. Acta 1218, 453-456, 1994
A:Title: Cloning and analysis of chicken acetylcholinesterase transcripts from
A:Reference number: S47639; MUID:94325359; PMID:8049273
A:Accession: S47639
A:Molecule type: mRNA
A:Residues: 1-767 <RAN>
A:Cross-references: UNIPROT:P36196; EMBL:U03472; NID:g623031; PIDN:AAA60456.1;
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase

Query Match	46.8%	Score 1455.5	DB 2	Length 767
Best Local Similarity	39.4%	Pred. No. 2.4e-103	Indels 173	Gaps 6
Matches 291	Conservative	87	Mismatches 188	
Qy	6	IATKNGKVRGMMNITV--FGGTVTAFGLGIPYAQPPLGRLRFRKKPOSQ-LTKNSDIWNATKYA	62	
Db	32	VRITTSVVRGLLIPAGPSGSTAAAFGLGIPFAVPLPLGRFRPPLPIPTPTWTGIRDADSQP	91	
Qy	63	NSSCQNTDQSPGPHGSEMNPNTDLSIEDCLYLNNWTPAPKPKNATVLINWYIGGGFQTGT	122	
Db	92	FACYQWYDITTFPGFQGSMMNPNNREMSIEDCLYLNNWTKGQDTPPPVLWYIGGGFTGGS	151	
Qy	123	SSLHVDYDGKFLARVERVIVVSMYRVYCALGFALPGNPEAPGNMGLFDQOOLALQWVKNI	182	
Db	152	VSLDVIDGRYLAAAEBAVVSMYRVYGSGLFALAGHRDAPGNVGLMDORLALQWRDNA	211	
Qy	183	AAFCGNPKSVTLFGESAGAAVSUHLHLSPGSHSLFTTRAILQSGSFNAPWATSVSYEARNR	242	
Db	212	EAFGQDPDLITLFGESAGAAVSVPGLHLSPHSKGLFRRAVLQSGSPNGPWATIGAAEGRRR	271	
Qy	243	TLNLAKLTGCSRENETELIIICLRANKDQOEILLNEAFVVPYCTPLSVNFGPVPVGDGLTDM	302	
Db	272	AAALGRVAGPCPYGNETEFGLGCLRKEAADVLEGGVGVNPPQSFVRFPFVVPVVDGDFVVD	331	
Qy	303	PDILLELQGF-----	312	
Db	332	PDVAL-WGDYGVKGGEGHGVGGDGGYGVKGGDGVKGGYGGYGARGVREGDGGGYGV	390	
Qy	313	-----	312	
Db	391	KEGLREGYGVKEGYVGEGBGANYGARVPPRPHRDETPPDAYGAKGSADAYGAKAAPRH	450	
Qy	313	-----KKT	315	
Db	451	RDETSPDAYGAKMPPRPHRDEASPDITGAKMPPRPHRDETSPDAYGAKMPPRPHRACGEV	510	
Qy	316	QILVGNVKNDEGTWFLVYGAPGFSKONNSIITRKEFQEGKLKIFPGVSEFGKESILFHYYD	375	

Db 511 EVLLGAVRVEGSLFYVGPFGKDNESLSREBFLGGVRMGVQATELAAEAVVLHYTD 570
Qy 376 WVDORPENYREALGDVVGDVNFICPALEFTTKKSEWGNNAFFYFHEHRSKSLPWPWMG 435
Db 571 WLDADNPVKNREALDDIVGDHNVVCPMAFAQRAQRAQKGVYALDFHRSSTLLWPMMG 630
Qy 436 VMHGYEIEFVGLPLERDDNTYTKABEILSRISVKKRWANFAKYGPNPNETQNNSTSWPVFKS 495
Db 631 VPHGYEIEFVGLPLERDDNTYTKABEILSRISVKKRWANFAKYGPNPNETQNNSTSWPVFKS 689
Qy 496 TEQKYLTINTSTRTIMTKLRAQOCRFWTSFPFKVLEMTGNIDEAEWENKAGFHRNNYMM 555
Db 690 SGQRYAHLNAPRLSVGHGLRTQICAFWTRFLPKLINATGPPDAERWLEFHRWSVMG 749
Qy 556 DWKQFNDYTSKKSCEVGL 574
Db 750 RWRTOFEHY-SRQOPCATL 767

RESULT 12
A54413
acetylcholinesterase (EC 3.1.1.7) A precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A54413; T29824
R:Arpagaus, M.; Fedon, Y.; Cousin, X.; Chatonnet, A.; Berge, J.B.; Fournier, D.; Tountas
J.; Biol. Chem. 269, 9957-9965, 1994
A:Title: cDNA sequence, gene structure, and in vitro expression of ace-1, the gene encoding
A:Reference number: A54413; MUID:94193691; PMID:8144590
C:Accession: A54413
A:Status: preliminary
A:Molecule type: mRNA
A:Cross-references: UNIPROT:P38433; GB:X75331; MID:g475060; PIDN:CAA53080.1; PID:g671831
A:Residues: 1-620 <R>
R:Wu, X.; Le, T.T.
A:Description: The sequence of C. elegans cosmid W09B12.
A:Reference number: Z20693
A:Accession: T29824
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-620 <WUX>
A:Cross-references: EMBL:U58731; PIDN:AAB00593.1; GSPDB:GN00028
A:Experimental source: strain Bristol N2; clone W09B12
C:Genetics:
A:Gene: CESP:ace-1
A:Map position: X
A:Introns: 13/3; 59/2; 236/3; 296/2; 454/2; 509/2; 573/1; 606/2
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase
F:45-567/Domain: cholinesterase homology <CHE>

Query Match 36.7%; Score 1142; DB 2; Length 620;
Best Local Similarity 41.0%; Pred. No. 1.9e-79;
Matches 243; Conservative 94; Mismatches 213; Indels 42; Gaps 14;

Qy 18 LTVFGTGTAFGLGIPYAPPLGRFRFKKPOSITKWSDIWNAKYANSCCNIDQSPGCFH 77
Db 35 LSQTKPLTRFQGLPFAEPVGNLGRFKPKQKWPRLNATTPNSQIBSEDTYFGDFY 94
Qy 78 GSEMNPNLTSDECLYLVNWIPIA---PKPKNATVLIWYGGGFTGTSSLHVYDGKFLA 134
Db 95 GSTMWNATKLSDECLYLVNVPKVDPNKKLA-VVMVYGGGWSGTATLDVYDGLIT 153
Qy 135 RVERVIVVMYRVGALGFALPGNPEAPGNMGLFDQOLALQWQKNIAPAGGNPKSVTL 194
Db 154 VEENVILVAMRYVSIFFGLYM-NRPEAPGNMGMWDLAMKWKHKNIDLFEGDLSRITL 212
Qy 195 FEGSAGASVSHLLSPGSHSLFTRAILQSGSFNAPWATVSLYEARNRTNLAKLTGCS- 253
Db 213 FEGSAGASVSHLLSPGSHSLFTRAILQSGSFNAPWATVSLYEARNRTNLAKLTGCS- 272
Qy 254 ----RENETEIKLRNKDPQOELLNE-AFVVVPYGTPLSVNFGPTVDGDFLTMDPDIILE 308

Db 273 MSLINPDYRLDDCFORADADALRENEWAPVREFG---DFPWPVVVDGDFLENAQTSLK 329
Qy 309 LGQPKTKTQIILVGNVKNDEGTWFLVYGAPGFKONNNSIITRKEFOEGLKIFPPGVSFEFKES 368
Db 330 QGNFKTKQLLAGSNRDESIYFLTYQLPDIFFVAD-FFTCTDFIKDROLWIKGVKDLLPRQ 388
Qy 369 IL-----PHYTDWVD-DQSPENYREALGDVVGDVNFICPALEFTTKKFSWGNNAFF 418
Db 389 ILKQLTLAAVLHEYEPQDLFVTPRDWINAMDWMLGDYHFTCSVNEMALAHTKHGGDTYY 448
Qy 419 YFEHRSKSLPWPBWMGVMHGYEIEFVGLPL-ERRDNYTKABEILSRISVKKRWANFAK 477
Db 449 YFTHRASQQTWPBWMGVLHGYELNFIFFGELQKRFNYTDEERELSNRRFMYWANFAKT 508
Qy 478 GNPNETQNNST---WPFVKSTQKYLTNTTEST-----RIMTKLRAQOCRFWTSFPFKV 529
Db 509 GDNPKNEDGSFTQDVWVPKYNVSVMYNTVSSYSPSMKRIGHGPRRKECAFWKAYLPNL 568
Qy 530 LEMTGNIDEAEWENKAGFHRW-NNYMMDWKNQFNDY-----TSKKESCVCV 573
Db 569 MAAVADVDPYLVWVKQMDRWQNEYITDWOYHFEQYKRYQTYRQSDSETCG 620

RESULT 13
S66236
acetylcholinesterase (EC 3.1.1.7) precursor - yellow fever mosquito
C:Species: Aedes aegypti (yellow fever mosquito)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66236
R:Anthony, N.; Rocheleau, T.; Mocelin, G.; Lee, H.J.; french-Constant, R.
FEBS Lett. 368, 461-465, 1995
A:Title: Cloning, sequencing and functional expression of an acetylcholinesterase gene f
A:Reference number: S66236; MUID:95361924; PMID:7635199
C:Accession: S66236
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-637 <ANT>
A:Cross-references: UNIPROT:Q9TX11
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-637/Product: acetylcholinesterase #status predicted <MAT>
F:57-594/Domain: cholinesterase homology <CHE>

Query Match 34.4%; Score 1070.5; DB 2; Length 637;
Best Local Similarity 38.9%; Pred. No. 6e-74;
Matches 223; Conservative 90; Mismatches 207; Indels 53; Gaps 8;

Qy 2 DDIIATKNGKVRGMNLTVFGGTVAFLGIPYAPPLGRFRFKKPOSITKWSDIWNAKY 61
Db 31 DRLVVQTSSGPIRGRTMVLGRVHVVPNGVYPAKPPVDGLRFRKFPVPAEPWHGVLDATRL 90
Qy 62 ANSCCNIDQSPGCFHSGSEMNPNLTSDECLYLVNWIPIA----- 101
Db 91 PPSCIOERYEYFFGFACEEMNPNLTVSDECLYLVNWIPIA----- 150
Qy 102 -----PKPKNATVLIWYGGGFTGTSSLHVYDGKFLARVERVIVVMYRVGALGF 153
Db 151 DDDPQROHQSGKGLAMLVVIYGGGFTGTSSLHVYDGKFLARVERVIVVMYRVGALGF 210
Qy 154 LALP---GNPEAPGNMGLFDQOLALQWQKNIAPAGGNPKSVTLFEGSAGASVSHLLS 210
Db 211 FYLAPYLNDDDAFCNVLGMDQALAIWLKENAKAFGDDPDLITLFGSAGSSVSHLLS 270
Qy 211 PGSHSLFTRAILQSGSFNAPWATVSLYEARNRTNLAKLTGCS----RENETEIKLRN 266
Db 271 PVTRGLSRRGILQSGTLNAPWHSMAEKALSAEALDDCNVTLKDKPNPYVMNCWRN 330
Qy 267 KDPQEILLNEAFVVPYGTPLSVNFGPTVDGDFLTMDPDIILELQFKTKTQIILVGNVKNDEG 326
Db 331 VDARTISVQO--WNSYSGILGFPSPAPTIDGVFMFTADPMTMLREANLEGVILVGSNDEG 388

